



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 19722

TO: Minh-Tam Davis
Location: rem/3A24/3C18
Art Unit: 1642
Friday, June 09, 2006

Case Serial Number: 09/743825

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Davis,

Here are the results for your recent search request.

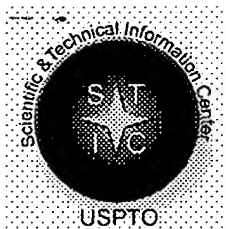
Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 187401

TO: Minh-Tam Davis
Location: rem/3A24/3C18
Art Unit: 1642
Thursday, May 04, 2006

Case Serial Number: 09/743825

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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7.3.6.28

187401

MS

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Thursday, April 27, 2006 10:52 AM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/743825

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

STIC
APR 27 2006
10:52 AM

-----Original Message-----

From: Davis, Minh-Tam
Sent: Thursday, April 27, 2006 10:15 AM
To: Chan, Christina
Subject: Rush search request for 09/743825

Please search for interference only:

- 1) SEQ ID NO:1.
- 2) Nucleotides 77-1753 of SEQ ID NO:1.
- 3) SEQ ID NO: 7, 8 and 10, with size limitation for the data in the database to the size of the corresponding sequences.

THANK YOU
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

Searcher: noble
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 5/15/06
Searcher Prep Time: 5
Online Time: 2

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Cambridge
WWW/Internet: _____
Other (Specify): _____

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73622

192 242

119

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Wednesday, June 07, 2006 1:36 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/743825

Please ~~push~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, June 07, 2006 1:32 PM
To: Chan, Christina
Subject: Rush search request for 09/743825

Please search in commercial database, issued patent files and PGPUB:
SEQ ID NO:7, 8, 10 with size limitation for the sequences in the database to the size of the corresponding sequences.
Thank you.

MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 00:36:21 ; Search time 289 Seconds
(without alignments)
482.509 Million cell updates/sec

Title: US-09-743-825-10
Perfect score: 20
Sequence: 1 gaccgcatagacttctcaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 2681012

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 8.*

- 1: Geneseqn1980a.*
- 2: Geneseqn1990a.*
- 3: Geneseqn2000a.*
- 4: Geneseqn2001a.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3 AAZ50446	AAZ50446 Human PB3
2	13.8	69.0	20	2 AAX93486	AAX93486 PCR prime
3	13.2	66.0	20	10 AAD62200	AAD62200 Human hae
4	12.6	63.0	19	15 AEE31152	AEE31152 Haemophil
5	12.6	63.0	20	13 ADT00440	ADT00440 Novel mut
6	12.6	63.0	20	14 ADW95798	ADW95798 Human TFR
7	12.6	63.0	20	14 ADZ44776	ADZ44776 Human tra
8	12.4	62.0	17	8 ACA08287	ACA08287 Necrosis
9	12.4	62.0	17	8 ACA06680	ACA06680 NFKB sub-
10	12.2	61.0	18	3 AAZ48549	AAZ48549 Human TNF
11	12.2	61.0	18	6 APT05045	APT05045 TNFR1 exp
12	12.2	61.0	18	13 ADR06077	ADR06077 Human TNF
13	12.2	61.0	19	10 ADG73193	ADG73193 Pseudomon
14	12.2	61.0	19	10 ADL12249	ADL12249 Pseudomon
15	12.2	61.0	20	12 ADI79866	ADI79866 Mouse HMG
16	12.2	61.0	20	12 ADI79673	ADI79673 Mouse HMG
17	12.2	61.0	20	14 ADW95797	ADW95797 Human TFR
18	12.2	61.0	20	14 ADX57319	ADX57319 Forward P

19	12.2	61.0	20	14 ADZ44775	ADZ44775 Human tra
20	12	60.0	20	2 AAQ32840	AAQ32840 Microsate
21	12	60.0	20	2 AAQ57863	AAQ57863 Primer pa
22	12	60.0	20	2 AAZ21763	AAZ21763 Exemplary
23	12	60.0	20	3 AAC60963	AAC60963 TATA box-
24	11.8	59.0	17	10 ADB42063	ADB42063 Tumour su
25	11.8	59.0	17	10 ADI48431	ADI48431 Human tum
26	11.8	59.0	18	2 AAQ94315	AAQ94315 Human cyt
27	11.8	59.0	18	2 AAV30475	AAV30475 Canine be
28	11.8	59.0	18	14 AEC47173	AEC47173 Antisense
29	11.8	59.0	18	14 AEC47021	AEC47021 Antisense
30	11.8	59.0	18	14 AEC47477	AEC47477 Antisense
31	11.8	59.0	18	14 AEC47325	AEC47325 Antisense
32	11.8	59.0	19	14 AEB50764	AEB50764 Human ADA
33	11.8	59.0	19	14 AEB50960	AEB50960 Human ADA
34	11.8	59.0	19	14 AEB22319	AEB22319 Liver fib
35	11.8	59.0	20	2 AAV33985	AAV33985 Primer CT
36	11.8	59.0	20	3 AAZ24116	AAZ24116 Primer CT
37	11.8	59.0	20	10 ABZ91284	ABZ91284 Human Oli
38	11.8	59.0	20	11 ABD27514	ABD27514 AA486238-
39	11.6	58.0	19	4 AAD11750	AAD11750 Human AAG
40	11.6	58.0	19	14 ADW79353	ADW79353 Human ace
41	11.6	58.0	19	14 ADW78939	ADW78939 Human ace
42	11.6	58.0	19	14 AEA11754	AEA11754 Human ACA
43	11.6	58.0	19	14 AEA11340	AEA11340 Human ACA
44	11.6	58.0	20	6 ABK41518	ABK41518 Human CTN
45	11.6	58.0	20	6 ABS59713	ABS59713 Human dam

ALIGNMENTS

RESULT 1

AAZ50446
ID AAZ50446 standard; DNA; 20 BP.

AC AAZ50446;

DT 18-MAY-2000 (first entry)

DE Human PB39 specific 3' RACE primer.

XX PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer;
KW prostate epithelium; splicing mechanism; early diagnosis; progression;
KW precancerous cell; metastatic potential; non-neoplastic prostate disease;
KW expressed sequence tag; EST; PCR primer; ss.

XX Homo sapiens.

XX WO200005376-A1.

PD 03-FEB-2000.

PF 23-JUL-1999; 99WO-US016831.

PR 24-JUL-1998; 98US-0094137P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Chuaqui RF, Cole KA, Liotta LA;

XX WPI; 2000-182700/16.

DR Novel gene which is dysregulated in prostate cancer useful for diagnosing cancer.

PS Claim 5; Page 18; 51pp; English.

XX The present sequence is the human PB39 3' specific RACE primer, from EST clone AAR00504. It is used to determine the complete nucleotide sequence of PB39 cDNA, isolated from human pancreas cDNA library using RACE. The PB39 gene that is dysregulated in prostate cancer has homology to the EST AAR00504. PB39 gene is located on chromosome 11p11.1-11.2. Abnormally

CC high concentrations of PB39 are found in prostate tissue derived from
 CC prostate cancer (PC) epithelium. PB39 sequence is useful for detection of
 CC precancerous or cancer cells in the prostate. PB39 is useful for early
 CC diagnosis of the progression of prostate cancer, especially in aggressive
 CC prostate carcinoma. It can also distinguish PC from other non-neoplastic
 CC prostate disease. The diagnostic method is selective and specific for
 CC various types of PC and also facilitates identifying prostate cancer of
 CC differing aggressiveness and metastatic potential

XX SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTTCTCAGA 20
 |||||
 DB 1 GACCGCATAGACTTCTCAGA 20

RESULT 2
 AAX93486
 ID AAX93486 standard; DNA; 20 BP.

XX AC AAX93486;

XX DT 13-SEP-1999 (first entry)

XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.

XX OS Synthetic.
 OS Chlamydia pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.

XX PI Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1595; Disclosure; 1912pp; English.

XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

XX SQ Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 20;
 Best Local Similarity 88.2%; Pred. No. 2.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTTCTC 17
 |||||
 DB 3 GACCGCATAAACTTATC 19

RESULT 3

AAD62200/c

ID AAD62200 standard; DNA; 20 BP.

XX AC AAD62200;

XX DT 15-JAN-2004 (first entry)

XX DE Human haematopoietic cell tyrosine kinase antisense oligo ISIS #150755.

XX KW Haematopoietic cell; tyrosine kinase; hyperproliferative disorder;
 KW cancer; therapy; inflammation; diabetes; viral infection; inflammation;
 KW tumour; cytostatic; virucide; antisense therapy; antisense; human;
 KW phosphorothioate backbone; ss.

XX OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone; All cytidines are 5-
 methyl cytidines"

FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"

XX US2003125275-A1.

XX 03-JUL-2003.

XX 04-DEC-2001; 2001US-00007010.

XX 04-DEC-2001; 2001US-00007010.

XX (ISIS-) ISIS PHARM INC.

XX Borchers AH, Dobie KW;

XX WPI; 2003-811000/76.

XX New antisense oligonucleotides targeted to nucleic acids encoding
 CC haematopoietic cell protein tyrosine kinase, useful for diagnosing or
 CC treating cancer (e.g. leukemia), inflammation, diabetes or viral
 CC infections.

XX Example 15; Page 26; 59pp; English.

XX The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding haematopoietic cell protein tyrosine kinase. The compound
 CC inhibits the expression of haematopoietic cell protein tyrosine kinase
 CC and it specifically hybridises with the nucleic acid molecule encoding
 CC the tyrosine kinase or with at least an 8-nucleobase portion of an active
 CC site on the nucleic acid molecule encoding the tyrosine kinase. The
 CC antisense compounds are useful for modulating the expression of
 CC haematopoietic cell protein tyrosine kinase and treating diseases or
 CC conditions associated with the expression of the tyrosine kinase, such as
 CC hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a
 CC viral infection. The antisense compounds are also useful for diagnostics,
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation, as research reagents and kits and in

CC distinguishing between functions of various members of a biological
CC pathway. The present sequence is human haematopoietic cell tyrosine
CC kinase antisense oligonucleotide
XX
XX Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
SQ Query Match 66.0%; Score 13.2; DB 10; Length 20;
Best Local Similarity 83.3%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ACCGCATAGACTTCTCAG 19
Db | | | | | | | | | | | | | | | | | | | |
20 AACTCATTGACTTCTCAG 3

RESULT 4
AEE31152/c
ID AEE31152 standard; DNA; 19 BP.
AC AEE31152;
XX
DT 09-FEB-2006 (first entry)
XX
DE Haemophilus influenzae trxB PCR primer.
XX
KW vaccine; antibacterial; trxB; PCR; primer; ss.
XX
OS Haemophilus influenzae.
XX
PN US2005272089-A1.
XX
PD 08-DEC-2005.
XX
PF 01-AUG-2005; 2005US-00194246.
XX
PR 19-OCT-2001; 2001US-0345438P.
PR 21-OCT-2002; 2002US-00274586.
XX
PA (MOTT/) MOTT J E.
PA (TREP/) TREP C M.
PA (ARVI/) ARVIDSON S.
XX
PI Mott JE, Trepod CM, Arvidson S;
XX
DR WPI; 2006-037204/04.
XX
XX Novel isolated polypeptide critical for survival of Haemophilus species,
PT useful for reducing virulence of H. influenzae to be used as vaccine
PT composition.
XX
PS Example 2; SEQ ID NO 121; 158pp; English.
XX
XX The invention relates to an isolated polypeptide (I) critical for the
CC survival of Haemophilus sp. comprising an amino acid sequence having at
CC least 95% structural similarity with an amino acid sequence chosen from
CC AEE31317, AEE31330, AEE31332, AEE31345, AEE31353, AEE31354 and
CC AEE31358. Also described: (1) an isolated polynucleotide (II) critical
CC for the survival of Haemophilus sp. comprising a nucleotide sequence
CC having at least 95% structural similarity with nucleotide sequence chosen
CC from a coding sequence in AEE31062, AEE31130, AEE31140, AEE31155,
CC AEE31211, AEE31241, AEE31246 and AEE31231, and its complements, and
CC encoding (1); (2) identifying (M1) an agent that binds a polypeptide,
CC involves combining a polypeptide and an agent to form a mixture, where
CC the polypeptide is encoded by a coding sequence comprising a nucleotide
CC sequence having at least 95% structural similarity with a nucleotide
CC sequence chosen from AEE31062, AEE31130, AEE31140, AEE31155, AEE31211,
CC AEE31241, AEE31246, AEE31263 and AEE31231, or has at least 95% structural
CC similarity with an amino acid sequence chosen from AEE31317, AEE31330,
CC AEE31332, AEE31335, AEE31345, AEE31353, AEE31354 and AEE31358, and
CC determining whether the agent binds the polypeptide; (3) decreasing the
CC growth rate of a microbe, involves combining a microbe with an agent that
CC binds to a polypeptide encoded by a coding sequence comprising a
CC nucleotide sequence chosen from AEE31062, AEE31130, AEE31140, AEE31155,

CC AEE31211, AEE31241, AEE31246, AEE31263 and AEE31231; (4) making (M2) an
CC H. influenzae with reduced virulence, which involves altering a coding
CC sequence in an H. influenzae to comprise a mutation, the non-mutagenized
CC coding sequence comprising a nucleotide sequence chosen from AEE31062,
CC AEE31130, AEE31140, AEE31155, AEE31211, AEE31241, AEE31246, AEE31263 and
CC AEE31231, and determining if the H. influenzae comprising the mutation
CC has reduced virulence compared to an H. influenzae that does not comprise
CC the mutation; (5) an H. influenzae obtained by (M2); and (6) a vaccine
CC composition comprising the H. influenzae. (I) is useful for reducing the
CC virulence of H. influenzae to be used as a vaccine composition, and for
CC decreasing the growth rate of a microorganism. The present sequence
CC represents a PCR primer for a H. influenzae trxB coding sequence, which
CC is used in the exemplification of the present invention.
XX
XX Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
SQ Query Match 63.0%; Score 12.6; DB 15; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ACCGCATAGACTTCTCAGA 20
Db | | | | | | | | | | | | | | | | | | | |
19 ACCGCTTACACTTTTCACA 1

RESULT 5
ADT00440
ID ADT00440 standard; DNA; 20 BP.
XX
AC ADT00440;
XX
DT 16-DEC-2004 (first entry)
XX
DE Novel mutant protein tyrosine kinase-related oligonucleotide SeqID428.
XX
KW tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW tumorigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW GUCY2F; MCKK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW guanylate cyclase stimulator; ss.
XX
OS Homo sapiens.
XX
PN WO2004082458-A2.
XX
PD 30-SEP-2004.
XX
XX 18-FEB-2004; 2004WO-US004452.
XX
XX 21-FEB-2003; 2003US-0448537P.
XX
XX 29-MAY-2003; 2003US-0473895P.
XX
XX (UWJO) UNIV JOHNS HOPKINS.
XX
XX Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;
XX WPI; 2004-718702/70.
XX
XX Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCKK) and
XX associated methods for diagnosing cancer and screening for anti-cancer
XX agents.
XX
XX Disclosure; SEQ ID NO 428; 363pp; English.
XX
XX This invention relates to a novel activated mutant protein tyrosine
XX kinases and associated methods for diagnosing cancer and screening for
XX anti-cancer agents. Protein kinases are signalling molecules involved in
XX tumorigenesis. Mutational analysis of the human tyrosine kinase gene
XX family identified somatic alteration in 1 in 5 colorectal cancers, with
XX the majority of mutations occurring in the NTRK3, FES, GUCY2F and
XX MCKK/MLK4 genes. Most were identified in the kinase domain. The invention
XX may be useful for the production of compounds with a cytostatic activity
XX acting as protein tyrosine kinase inhibitors or guanylate cyclase
XX stimulators. The invention may be useful for developing methods for

CC detecting mutations involved in cancer or screening for anti-cancer
 CC agents. The present sequence is that of a human-derived oligonucleotide
 CC which is related to the invention.

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 13; Length 20;

Best Local Similarity 78.9%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACCGCATAGACTTCTCAG 19

Db 2 GACCCGCTAGTCATCTCAG 20

RESULT 6

ADW95798

ID ADW95798 standard; DNA; 20 BP.

AC ADW95798;

DT 07-APR-2005 (first entry)

DE Human TFR cDNA 424A allele specific biotin-labeled 5' oligo, TFRd1.G.

XX diagnosis; pharmaceutical; iron overload; toxicity; intoxication;
 KW disorder of iron metabolism; hemochromatosis; cardiant; hepatotropic;
 KW metabolic disorder; gene therapy; TFR; transferrin receptor; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Biotin-labeled"

XX US6849399-B1.

PD 01-FEB-2005.

PP 27-AUG-1997; 97US-00920559.

XX 23-MAY-1996; 96US-00652265.

PR 04-APR-1997; 97US-00834497.

PR 13-JUN-1997; 97US-00866211.

XX (BIRA) BIO-RAD LAB INC.

PI Feder JN, Schatzman RC, Tsuchihashi Z;

XX WPI; 2005-129963/14.

PT Diagnosing hereditary hemochromatosis, involves providing sample
 PT comprising patient's nucleic acid, detecting presence or absence of A424G
 PT allele of polymorphism in nucleic acid that encodes transferrin receptor.

XX Claim 4; SEQ ID NO 12; 29pp; English.

XX The present invention relates to methods and compositions for the
 CC diagnosis and treatment of iron misregulation diseases including HFE
 CC polypeptides and the polynucleotides encoding them. The iron
 CC misregulation diseases include both iron overload diseases and iron
 CC deficiency diseases. The invention is useful for diagnosing hereditary
 CC hemochromatosis and in gene therapy. The present sequence is human
 CC transferrin receptor (TFR) cDNA 424A allele specific biotin-labeled
 CC oligonucleotide. This oligonucleotide is used in the screening for A424G
 CC polymorphism in the hereditary hemochromatosis patient chromosomes.

SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 14; Length 20;

Best Local Similarity 78.9%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACCGCATAGACTTCTCAG 19

Db 2 GACAGCACAGACTTCACCG 20

RESULT 7

ADZ44776

ID ADZ44776 standard; DNA; 20 BP.

XX ADZ44776;

DT 14-JUL-2005 (first entry)

DE Human transferrin receptor OLA oligonucleotide TFRd1.G SEQ ID NO:12.

XX hemochromatosis; cardiant; hepatotropic; transferrin receptor; ss.

OS Homo sapiens.

OS Synthetic.

PN US2005090430-A1.

XX 28-APR-2005.

PD 01-OCT-2004; 2004US-00956250.

PP 23-MAY-1996; 96US-00652265.

PR 04-APR-1997; 97US-00834497.

PR 13-JUN-1997; 97US-00866211.

PR 27-AUG-1997; 97US-00920559.

XX (BIRA) BIO-RAD LAB INC.

XX Feder JN, Schatzman RC, Tsuchihashi Z;

XX WPI; 2005-331970/34.

PT Treatment of hemochromatosis in a patient involves administering HFE (HLA
 PT -H) polypeptide to the patient.

XX Example; SEQ ID NO 12; 26pp; English.

XX The invention relates to a method of treating hemochromatosis in a
 CC patient by administering the hemochromatosis protein HFE (HLA-H) to the
 CC patient. The method is used for treating hemochromatosis. The invention
 CC provides a molecular basis for the relationship of HFE to iron metabolism
 CC and diagnostic and therapeutic agents for the treatment of iron
 CC misregulation diseases. The present sequence represents an
 CC oligonucleotide ligation assay (OLA) oligonucleotide for the human
 CC transferrin receptor, which is used in an example from the present
 CC invention.

SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 14; Length 20;

Best Local Similarity 78.9%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACCGCATAGACTTCTCAG 19

Db 2 GACAGCACAGACTTCACCG 20

RESULT 8

ACA08287

ID ACA08287 standard; DNA; 17 BP.

XX ACA08287;

XX 03-JUN-2003 (first entry)

XX

DE Necrosis factor kappa B (NFkB) sub-unit modulating DNazyme #56.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;
 KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
 KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
 KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
 KW multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;
 KW paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;
 KW doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;
 KW radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Synthetic.

OS US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

PI WPI; 2003-340953/32.

DR Novel enzymatic nucleic acid molecules which down regulates expression of
 XX a sequence encoding a subunit of nuclear factor kappa B useful for
 XX treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 46; 72pp; English.

CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents an enzymatic nucleic acid used to
 CC modulate the function of a necrosis factor kappa B sub-unit

XX Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

XX Query Match 62.0%; Score 12.4; DB 8; Length 17;
 XX Best Local Similarity 64.3%; Pred. No. 1.5e+04;
 XX Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 CATGACTTCTCAG 19
 ||: |||::|||
 DB 4 CAUGGACUUCUCAG 17

RESULT 9
 ACA06680
 ID ACA06680 standard; RNA; 17 BP.
 AC ACA06680;
 XX
 XX 03-JUN-2003 (first entry)
 DT
 DE NFkB sub-unit modulating inozyme substrate #499.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

OS US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

PI WPI; 2003-340953/32.

DR Novel enzymatic nucleic acid molecules which down regulates expression of
 XX a sequence encoding a subunit of nuclear factor kappa B useful for
 XX treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 34; 72pp; English.

CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents an enzymatic nucleic acid used to
 CC modulate the function of a necrosis factor kappa B sub-unit


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XX KW cytostatic; gene therapy; apoptosis inhibitor;
XX KW radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;
XX KW human; antisense oligonucleotide; antisense technology; ss.
XX OS Homo sapiens.
XX FH Key
XX FT modified_base 1. .18 Location/Qualifiers
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT modified_base 1. .4
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT 17-JUN-1999; 98US-00106038.
XX FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
XX FT nucleotides"
XX FT modified_base 15. .18
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
XX FT nucleotides"
XX PN US2004147471-A1.
XX PD 29-JUL-2004.
XX PP 06-NOV-2003; 2003US-00702817.
XX PR 26-JUN-1998; 98US-00106038.
XX PR 17-JUN-1999; 99WO-US013763.
XX PR 24-OCT-2000; 2000US-00695451.
XX PA (ZHAN/) ZHANG H.
XX PI Zhang H;
XX PI Zhang H;
XX DR WPI; 2004-561407/54.
XX XX Inhibiting radiation-induced apoptosis in a cell or tissue comprises
XX FT administering to the cell or tissue an antisense oligonucleotide targeted
XX FT to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
XX PS Example 10; SEQ ID NO 75; 24pp; English.
XX CC The invention describes a method of inhibiting radiation-induced
XX CC apoptosis in a cell or tissue comprising administering to the cell or
XX CC tissue an antisense oligonucleotide of 8-30 nucleotides in length
XX CC targeted to a nucleic acid molecule encoding tumour necrosis factor
XX CC receptor 1 (TNFR1). The method and antisense oligonucleotides are useful
XX CC for inhibiting radiation-induced apoptosis in a cell or tissue, and for
XX CC treating diseases associated with the expression of TNFR1. This sequence
XX CC represents a human tumour necrosis factor receptor 1 (TNFR1) antisense
XX CC oligonucleotide.
XX SQ Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
XX Query Match 61.0%; Score 12.2; DB 13; Length 18;
XX Best Local Similarity 82.4%; Pred. No. 1.9e+04;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 4 CGCATAGACTTCTCAGA 20
XX DB 18 CGCCCGACTTCTCTCAGA 2
XX RESULT 13
XX ADG73193
XX ID ADG73193 standard; DNA; 19 BP.
XX AC ADG73193;
XX XX 11-MAR-2004 (first entry)
XX DT

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XX DE Pseudomonas syringae pv. tomato DC3000 Hop gene PCR primer #40.
XX KW Avr; Hop; transgenic plant; disease resistance; cancer; bacteria;
XX KW metabolic pathway; eukaryotic cell death; programmed cell death;
XX KW cytostatic; PCR; primer; ss.
XX OS Pseudomonas syringae; pv. tomato str. DC3000.
XX PN US2003204868-A1.
XX PD 30-OCT-2003.
XX PP 12-FEB-2003; 2003US-00365742.
XX PR 12-FEB-2002; 2002US-0356408P.
XX PR 10-MAY-2002; 2002US-0380185P.
XX PA (COLL/) COLLIER A.
XX PA (ALFA/) ALFANO J R.
XX PA (CART/) CARTINHOOR S W.
XX PA (SCHN/) SCHNEIDER D J.
XX PA (TANG/) TANG X.
XX PI Collmer A, Alfano JR, Cartinhour SW, Schneider DJ, Tang X;
XX DR WPI; 2003-875735/81.
XX XX New nucleic acid, useful in imparting disease resistance to a plant or in
XX FT preparing a composition for treating cancer.
XX PS Example; SEQ ID NO 187; 209pp; English.
XX CC The present invention relates to the isolation of Pseudomonas syringae
XX CC pv. tomato DC3000 Avr/Hop proteins, and the polynucleotide sequences
XX CC encoding them. Also disclosed are expression vectors, host cells, and
XX CC transgenic plants comprising polynucleotide sequences of the invention.
XX CC The polynucleotide and polypeptide sequences are useful in imparting
XX CC disease resistance to a plant or in preparing a composition for treating
XX CC cancer. The sequences may also be used to make a plant hypersusceptible
XX CC to colonisation by nonpathogenic bacteria, modify a metabolic pathway in
XX CC a cell, cause eukaryotic cell death, and inhibit programmed cell death.
XX CC The present sequence represents a PCR primer used in the examples of the
XX CC present invention.
XX SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
XX Query Match 61.0%; Score 12.2; DB 10; Length 19;
XX Best Local Similarity 82.4%; Pred. No. 1.9e+04;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 3 CCGCATAGACTTCTCAG 19
XX DB 3 CCGCATAGACTTCTCTG 19
XX RESULT 14
XX ADL12249
XX ID ADL12249 standard; DNA; 19 BP.
XX AC ADL12249;
XX XX 06-MAY-2004 (first entry)
XX DE Pseudomonas syringae anti-cancer gene primer #60.
XX KW cytostatic; gene therapy; Avr; Hop; cancer; primer; ss.
XX KW Pseudomonas syringae; pv tomato DC3000.
XX OS WO2003068930-A2.
XX PN WO2003068930-A2.
XX XX 21-AUG-2003.
XX PD

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XX 12-FEB-2003; 2003WO-US004450.
XX PF
XX 12-FEB-2002; 2002US-0356408P.
XX PR
XX 10-MAY-2002; 2002US-0380185P.
XX XX
XX (CORR ) CORNELL RES FOUND INC.
XX PA (USDA ) US SEC OF AGRIC.
XX PA (UYNE-) UNIV NEBRASKA.
XX PA (UNIV ) UNIV KANSAS STATE RES FOUND.
XX PI
XX Collmer A, Alfano JR, Cartinhour SW, Schneider DJ, Tang X;
XX WPI; 2003-679632/64.
XX DR
XX New nucleic acid molecule, useful for preparing a composition for
XX PT treating cancer.
XX PT
XX Disclosure; SEQ ID NO 187; 284pp; English.
XX PS
XX The invention relates to novel Pseudomonas Avr and Hop genes, a sequence
XX CC that hybridizes with these sequences under stringency conditions
XX CC comprising a hybridization medium that includes 0.9 x saline sodium
XX CC citrate (SSC) buffer at a temperature of 42 deg C. The nucleic acid
XX CC molecule is useful for preparing a composition for treating cancer. This
XX CC sequence corresponds to a PCR to isolate and amplify one of the genes of
XX CC the invention.
XX CC
XX Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 61.0%; Score 12.2; DB 10; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CGCATAGACTTCTCAG 19
DB 3 CGCATAGACTTCTG 19
RESULT 15
ADI79866
ID ADI79866 standard; DNA; 20 BP.
XX AC
XX ADI79866;
XX DT 22-APR-2004 (first entry)
XX DE
XX Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID NO 389.
XX KW HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
XX KW HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaeamic;
XX KW antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
XX KW mouse; murine; ss.
XX OS
XX Mus musculus.
XX PN US2004006031-A1.
XX PD 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00190366.
XX PR
XX 02-JUL-2002; 2002US-00190366.
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX Dean NM, Freier SM, Dobie KW;
XX WPI; 2004-081743/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding HMG-CoA reductase, useful for treating
XX PT atherosclerosis, or a disease involving cholesterol metabolism or
```

```
PT angiogenesis.
XX XX
XX Example 16; SEQ ID NO 389; 110pp; English.
XX CC
XX The invention relates to novel compounds of 8-80 nucleobases in length
XX CC targeted to, and which specifically hybridizes with, a nucleic acid
XX CC molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
XX CC reductase, and inhibits the expression of HMG-CoA reductase. The novel
XX CC compounds have cardiant, antiarteriosclerotic, and antilipaeamic
XX CC activities. The compound can be used to treat disorders by antisense gene
XX CC therapy. The compounds, compositions and methods are useful for treating
XX CC a disease or condition associated with HMG-CoA reductase, such as a
XX CC cardiovascular disorder e.g. atherosclerosis, or a disease or condition
XX CC involving cholesterol metabolism. They are also useful in research and
XX CC diagnostics for modulating the expression of HMG-CoA reductase. This
XX CC polynucleotide sequence represents an antisense oligonucleotide of the
XX CC invention.
XX SQ
XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 61.0%; Score 12.2; DB 12; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 CGCATAGACTTCTCAGA 20
DB 3 CACAGAGACTCTCTAGA 19
Search completed: June 9, 2006, 00:41:31
Job time : 293 secs
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 23:02:12 ; Search time 289 Seconds
(without alignments)
506.634 Million cell updates/sec

Title: US-09-743-825-8
Perfect score: 21
Sequence: 1 ctggcgatctgaagagctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 3050480

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 8:*

- 1: Geneseqn1980a:*
- 2: Geneseqn1990a:*
- 3: Geneseqn2000a:*
- 4: Geneseqn2001a:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*
- 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	3	AZ50445 EST R0050
C 2	14	66.7	21	13	ADU41462
C 3	13.8	65.7	20	12	ADJ85951 Nucleic a
C 4	13.6	64.8	20	2	AZ05689 PCR prime
C 5	13.2	62.9	20	14	AEC30315 Human loc
C 6	13	61.9	20	4	AAC63691 Rat P2X ₇
C 7	13	61.9	20	9	ADA09833 Antisense
C 8	12.8	61.0	17	2	AAV97668 Human EGF
C 9	12.8	61.0	20	12	ADJ85562 Nucleic a
C 10	12.8	61.0	20	12	ADK96254 Primer of
C 11	12.8	61.0	21	10	ADF50105 Human BCL
C 12	12.8	61.0	21	10	ADF50117 Human BCL
C 13	12.8	61.0	21	10	ADF50125 Human BCL
C 14	12.8	61.0	21	10	ADF50109 Human BCL
C 15	12.8	61.0	21	10	ADG29696 BCL2-targ
C 16	12.8	61.0	21	10	ADG29693 BCL2-targ
C 17	12.8	61.0	21	10	ADG29700 BCL2-targ
C 18	12.8	61.0	21	14	ADV65888 Antisense

19	12.8	61.0	21	14	ADV65807 Sense str
C 20	12.4	59.0	19	12	ADQ61043 Anti-FRX
C 21	12.4	59.0	20	12	ADI79541 Human HMG
C 22	12.4	59.0	20	12	ADI79738 Human HMG
C 23	12.4	59.0	21	14	ACL49676 HAVCR1 si
C 24	12.4	59.0	21	14	ACL49850 HAVCR1 si
C 25	12.4	59.0	21	14	ACL49849 HAVCR1 ta
C 26	12.4	59.0	21	14	ACL49851 HAVCR1 si
C 27	12.4	59.0	21	14	ACL49678 HAVCR1 ta
C 28	12.2	58.1	17	2	AAV97669 Human EGF
C 29	12.2	58.1	17	8	ADB02331 Human MDZ
C 30	12.2	58.1	20	2	AAV29903 3' PCR pr
C 31	12.2	58.1	20	2	AAV31711 Kaposi's
C 32	12.2	58.1	20	10	AD61207 Human Shi
C 33	12.2	58.1	20	12	ADH50671 Human IRA
C 34	12.2	58.1	21	14	ADV87053 Mouse Myo
C 35	12.2	57.1	17	10	ADI50969 Human tum
C 36	12	57.1	20	4	AAC92623 Human nuc
C 37	12	57.1	20	12	ADP68593 Human PPA
C 38	12	57.1	20	12	ADP68748 Human PPA
C 39	12	57.1	20	14	ADX03575 Antisense
C 40	12	57.1	21	3	AAA46172 PCR prime
C 41	12	57.1	21	4	AAF97151 Human gen
C 42	12	57.1	21	13	AEA88036 Human lup
C 43	12	57.1	21	14	ADY21139 Human nes
C 44	11.8	56.2	17	2	AAQ51964 BCL-2 mRNA
C 45	11.8	56.2	17	2	AAV97667 Human EGF

ALIGNMENTS

RESULT 1
AAZ50445
ID AAZ50445 standard; DNA; 21 BP.

XX AC AAZ50445;

XX DT 18-MAY-2000 (first entry)

XX DE EST R00504-specific primer 2.

XX KW PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer;
prostate epithelium; splicing mechanism; early diagnosis; progression;
precancerous cell; metastatic potential; non-neoplastic prostate disease;
expressed sequence tag; EST; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200005376-A1.

XX PD 03-FEB-2000.

XX PF 23-JUL-1999; 99WO-US016831.

XX PR 24-JUL-1998; 98US-0094137P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Chuaqui RF, Cole KA, Liotta LA;

XX DR WPI; 2000-182700/16.

XX PT Novel gene which is dysregulated in prostate cancer useful for diagnosing cancer.

XX PS Claim 5; Page 16; 51pp; English.

XX CC The present sequence is the EST AAR00504-specific PCR primer, used for amplification of sequences contained within the EST AAR00504. It is useful to probe the gene overexpressed in prostate cancer epithelium and to analyse the differential expression of the EST. The PB39 gene that is dysregulated in prostate cancer is isolated from human pancreas cDNA

CC library and has homology to the EST AAR00504. PB39 gene is located on
 CC chromosome 11p11.1-11.2. Abnormally high concentrations of PB39 are found
 CC in prostate tissue derived from prostate cancer (PC) epithelium. PB39
 CC sequence is useful for detection of precancerous or cancer cells in the
 CC prostate. PB39 is useful for early diagnosis of the progression of
 CC prostate cancer, especially in aggressive prostate carcinoma. It can also
 CC distinguish PC from other non-neoplastic prostate disease. The diagnostic
 CC method is selective and specific for various types of PC and also
 CC facilitates identifying prostate cancer of differing aggressiveness and
 CC metastatic potential
 CC
 XX
 SQ Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGCGTATCTGAGAGTCTG 21
 Db 1 CTGGCGTATCTGAGAGTCTG 21

RESULT 2
 ADU41462/c

ID ADU41462 standard; DNA; 21 BP.

AC ADU41462;

XX 27-JAN-2005 (first entry)

DE Knock-down target sequence #6641.

XX ds; RNA production; protein production; drug development;
 KW knock-down target.

XX Unidentified.

XX WO2004094636-A1.

XX 04-NOV-2004.

XX 24-APR-2003; 2003WO-EP004362.

XX 24-APR-2003; 2003WO-EP004362.

XX (GALA-) GALAPAGOS GENOMICS NV.

PA (VSC/) VAN DER SCHUREN J.

XX Arts GJF, Lambrecht MJY, Djokic K, Clasen RU, Mesic B;

PI Griffioen S, Bergs CJL;

XX WPI; 2004-775940/76.

XX New knockdown sequences, useful in lowering the amount of RNA and/or
 PT protein production in cells used in drug development process.

XX Claim 11; SEQ ID NO 6678; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The
 CC polynucleotides, vector, libraries, and method are useful in lowering the
 CC amount of RNA and/or protein production in cells used in drug development
 CC process. The present sequence represents a knock-down target sequence.

XX Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 66.7%; Score 14; DB 13; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGCGTATCTGAAG 15

Db 16 TGGCGTATCTGAAG 3

RESULT 3

ADJ85951/c

ID ADJ85951 standard; DNA; 20 BP.

XX AC ADJ85951;

XX 06-MAY-2004 (first entry)

XX Nucleic acid analysis-related Tag probe SeqID1019.

XX restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
 KW T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
 KW assay development; product development; product validation;
 XX quality control; probe; ss.

XX Synthetic.

OS Unidentified.

XX WO2004007684-A2.

XX 22-JAN-2004.

XX 14-JUL-2003; 2003WO-US021990.

XX 12-JUL-2002; 2002US-0395530P.

XX (AFFY-) AFFYMETRIX INC.

XX Christians FC;

XX WPI; 2004-122923/12.

XX New DNA molecules made by annealing and extending overlapping 60mer
 PT oligonucleotides, useful in producing synthetic Tag genes useful as assay
 PT controls, in assay development, product development and for quality
 PT control.

XX Disclosure; SEQ ID NO 1019; 91pp; English.

XX This invention relates to a novel DNA molecule which comprises a DNA
 CC molecule made up of the following elements in a 5' to 3' direction: a
 CC first restriction endonuclease site; a T3 promoter site; at least one Tag
 CC gene comprising at least 5 20mer Tag sequences; a Poly A site having at
 CC least 21 consecutive A residues; a second restriction endonuclease site
 CC which may be the same or different than the first restriction
 CC endonuclease site; or a T7 Promoter on the opposite strand as the T3
 CC promoter. The invention may be useful in nucleic acid analysis, in
 CC particular to synthetic Tag genes useful as assay controls, in assay
 CC development, product development and validation and for quality control.
 CC The present sequence is that of a Tag oligonucleotide probe which may be
 CC used during the creation of the novel DNA molecule of the invention.

XX Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 12; Length 20;

Best Local Similarity 88.2%; Pred. No. 4.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGTATCTGAGAGTCTG 21

Db 20 CATATCTGGAGAGTCTG 4

RESULT 4

AAZ05689/c

ID AAZ05689 standard; DNA; 20 BP.

XX AC AAZ05689;

XX 07-OCT-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
OS Synthetic.
OS Chlamydia trachomatis.
XX WO9928475-A2.
XX 10-JUN-1999.
PD 27-NOV-1998; 98WO-IB001939.
XX 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX (GEST) GENSET.
XX Griffais R;
XX WPI; 1999-371125/31.
DR Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1791; 1755pp; English.
XX PCR primers AA201426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis;
CC epididymitis; cervicitis; salpingitis; perihepatitis; bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 64.8%; Score 13.6; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 TGGCGTATCTGAAGAGTCTG 21
DB 20 TGTGTTTCAGAGAGGCTG 1
RESULT 5
AEC30315/c
ID AEC30315 standard; DNA; 20 BP.
XX
AC AEC30315;
XX
XX 17-NOV-2005 (first entry)
XX
XX Human locus-specific oligonucleotide #1603.
XX
KW Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP;
KW major histocompatibility complex; MHC; HLA; human leukocyte antigen;
KW immune disorder; inflammation; inflammatory bowel disease;
KW ulcerative colitis; Crohn's disease; rheumatoid arthritis; diabetes;
KW diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;
KW Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;
KW rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;
KW dermatomyositis; pernicious anemia; primary biliary cirrhosis;
KW idiopathic thrombocytopenia purpura; Sjogren's syndrome;
KW multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;

KW gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive;
KW antiarthritic; antirheumatic; antidiabetic; muscular-gen.;
KW neuroprotective; dermatological; antithyroid; hepatotropic; antianemic;
KW hemostatic; opthalmological; uropathic; antipsoriatic; ss;
KW SNP detection.
XX Homo sapiens.
XX WO2005082110-A2.
XX 09-SEP-2005.
XX 28-FEB-2005; 2005WO-US006628.
XX 26-FEB-2004; 2004US-0547823P.
XX (ILLU-) ILLUMINA INC.
XX Oliphant A, Murray S;
XX WPI; 2005-638856/65.
XX Identifying single nucleotide polymorphism (SNP) haplotype that
PT correlates with the HLA type, useful for diagnosing an immunological or
PT inflammatory condition, comprises providing SNPs in the major
PT histocompatibility complex region.
XX
PS Example 1; SEQ ID NO 6335; 175pp; English.
XX The invention relates to a method of identifying the nucleotide for each
CC of a set of single nucleotide polymorphisms (SNPs) in the major
CC histocompatibility complex (MHC) region in a population of individuals,
CC comprising providing the HLA type for the individuals and identifying an
CC SNP haplotype in the population that correlates with the HLA type, where
CC the SNP haplotype comprises the SNPs in the MHC region. The invention
CC also relates to a method of predicting the HLA type of an individual, a
CC method of determining the presence or absence of an allelic variant of an
CC MHC gene in an individual, a method of identifying an SNP haplotype that
CC correlates with susceptibility to a disease or condition, and a method of
CC determining the susceptibility of an individual to a disease or
CC condition. The disease or condition is an immune disorder or inflammatory
CC condition selected from inflammatory bowel disease, ulcerative colitis,
CC Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,
CC myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,
CC Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic
CC lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,
CC pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia
CC purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and
CC psoriasis. This sequence represents a human locus-specific
CC oligonucleotide used in the scope of the invention.
XX
SQ Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 62.9%; Score 13.2; DB 14; Length 20;
Best Local Similarity 83.3%; Pred. No. 8.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CTGGCGTATCTGAAGAGT 18
DB 20 CTGGCGTATATGGAGAGT 3
RESULT 6
AAC63691
ID AAC63691 standard; DNA; 20 BP.
XX
AC AAC63691;
XX
XX 13-FEB-2001 (first entry)
XX
XX Rat P2X₇/P2Z PCR primer #3.
XX
XX Rat; P2X₇; neuroprotective; nontropic; antiinflammatory; antirheumatic;

KW antiarthritic; antibacterial; antiviral; antiallergic; cytostatic;
 KW cardiant; cerebroprotective; immunosuppressive; P2Z; purinergic receptor;
 KW nervous system disorder; chronic inflammation; Alzheimer's disease;
 KW rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection;
 KW haematopoietic system disorder; immune response; autoimmune disorder;
 KW allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
 KW tuberculosis; PCR primer; ss.

XX Rattus sp.

XX US6133434-A.

XX 17-OCT-2000.

XX 28-APR-1997; 97US-00842079.

XX 28-APR-1997; 97US-00842079.

XX (GLAX) GLAXO GROUP LTD.

XX Buell GN, Kawashima E, Surprenant A;

XX WPI; 2001-006153/01.

XX Mammalian purinergic receptor (P2X7) useful for screening for modulators
 PT which are useful for treating arthritic, respiratory disorders and
 PT neurodegenerative disorders, and to generate receptors specific
 PT antibodies.

XX Example 1; Col 7-8; 40pp; English.

XX The present invention relates to rat and human purinergic receptor
 CC P2X₇/P2Z (AAC63693-C63694). The P2X₇ coding sequences can be used to
 CC treat disorders of the nervous system, particularly diseases with a
 CC component of chronic inflammation, such as Alzheimer's disease, diseases
 CC involving acute or chronic inflammation such as rheumatoid arthritis,
 CC amyloidosis, bacterial, viral and other microbial infections, disorders
 CC of the haematopoietic system and immune response such as autoimmune
 CC disorders, allergies and lymphoproliferative disorders, diseases
 CC involving apoptotic cell death, such as cardiac and cerebral ischaemia
 CC and microbial infections, particularly tuberculosis. The present sequence
 CC is a PCR primer used to isolate the rat P2X₇ coding sequence

XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCCTATCTGAAG 15

Db 1 GGCCTATCTGAAG 13

RESULT 7

ADA09833

ID ADA09833 standard; DNA; 20 BP.

AC ADA09833;

XX 06-NOV-2003 (first entry)

XX Antisense nested PCR primer #1 for amplification of rat P2X₇ (P2Z).

XX PCR; ss; primer; permeabilising activity; P2X₇ receptor; P2Z receptor;
 KW receptor; ATP; antigen presenting cell; T lymphocyte;
 KW mitogenic stimulation; multinucleated giant cell; adenosine triphosphate;
 KW 3'-O-(4-benzoyl)benzoyl ATP; BzATP; fluorescent dye; propidium iodide;
 KW neutrotropic; neuroprotective; immunosuppressive; cerebroprotective;
 KW vasotropic; arthritic disorder; respiratory disorder;
 KW neurodegenerative disease; Alzheimer's disease; inflammation;
 KW rheumatoid arthritis; amyloidosis; infection; tuberculosis;
 KW haematopoietic system; immune response; allergy;

KW lymphoproliferative disorder; apoptosis; ischaemia; rat;
 KW autoimmune disorder.

XX Rattus sp.

XX US6509163-B1.

XX 21-JAN-2003.

XX 15-AUG-2000; 2000US-00638857.

XX 28-APR-1997; 97US-00842079.

XX (GLAX) GLAXO GROUP LTD.

XX Buell GN, Surprenant A, Kawashima E;

XX WPI; 2003-502654/47.

XX Screening of compound for its ability to modulate permeabilizing activity
 PT of mammalian receptor useful for treating e.g. arthritis, and Alzheimer's
 PT disease.

XX Example 1; SEQ ID NO 3; 43pp; English.

XX The invention discloses a method for screening a compound for its ability
 CC to modulate the permeabilising activity of a mammalian P2X₇ (P2Z)
 CC receptor. The P2Z receptor is a cell surface receptor for ATP and has
 CC been implicated in the lysis of antigen presenting cells by cytotoxic T
 CC lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well
 CC as in the formation of multinucleated giant cells. The preferred agonist
 CC is adenosine triphosphate (ATP) or 3'-O-(4-benzoyl)benzoyl ATP (BzATP)
 CC and the preferred method comprises monitoring the uptake into the cell of
 CC a detectable molecule, preferably a fluorescent dye (e.g. propidium
 CC iodide). The inventive method is useful for screening a compound for its
 CC ability to modulate the permeabilising activity of a mammalian P2X₇
 CC receptor useful for treatment of arthritic and respiratory disorders and
 CC neurodegenerative diseases. It is particularly useful in the treatment of
 CC Alzheimer's disease, diseases involving acute or chronic inflammation
 CC including rheumatoid arthritis, amyloidosis, bacterial, viral and other
 CC microbial infections, e.g. tuberculosis, disorders of the haematopoietic
 CC system and immune response, including autoimmune disorders, allergies and
 CC lymphoproliferative disorders, diseases involving apoptotic cell death,
 CC such as cardiac and cerebral ischaemia. The sequence presented is a
 CC nested PCR primer used for the amplification of rat P2X₇ cDNA.

XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCCTATCTGAAG 15

Db 1 GGCCTATCTGAAG 13

RESULT 8

AAV97668/c

ID AAV97668 standard; RNA; 17 BP.

XX AAV97668;

XX 17-MAR-1999 (first entry)

XX Human EGF-R target sequence nucleotide position 3858.

XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.

XX Homo sapiens.

XX

PN WO9833893-A2.
 XX 06-AUG-1998.
 XX 14-JAN-1998; 98WO-US000730.
 PF 31-JAN-1997; 97US-0036476P.
 XX 04-DEC-1997; 97US-00985162.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (UYAS-) UNIV ASTON.
 XX Akhtar S, Fell P, Mcswiggen JA;
 XX WPI; 1998-437449/37.
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 XX Claim 5; Page 77; 109pp; English.
 XX The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
 Query Match 61.0%; Score 12.8; DB 2; Length 17;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 GTATCTGAAGAGTCTG 21
 Db 16 GTATCGAAGAGTCTG 1
 RESULT 9
 ID ADJ85562/c
 XX ADJ85562 standard; DNA; 20 BP.
 AC ADJ85562;
 XX 06-MAY-2004 (first entry)
 DT Nucleic acid analysis-related Tag probe SeqID630.
 XX restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
 KW T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
 KW assay development; product development; product validation;
 KW quality control; probe; ss.
 XX Synthetic.
 OS Unidentified.
 XX WO2004007684-A2.
 XX 22-JAN-2004.
 XX 14-JUL-2003; 2003WO-US021990.
 XX 12-JUL-2002; 2002US-0395530P.
 XX (APFY-) APFYMETRIX INC.
 PI Christians FC;
 DR WPI; 2004-122923/12.
 XX New DNA molecules made by annealing and extending overlapping 60mer
 PT oligonucleotides, useful in producing synthetic Tag genes useful as assay
 PT controls, in assay development, product development and for quality
 PT control.
 XX Disclosure; SEQ ID NO 630; 91pp; English.
 PS This invention relates to a novel DNA molecule which comprises a DNA
 CC molecule made up of the following elements in a 5' to 3' direction: a
 CC first restriction endonuclease site; a T3 promoter site; at least one Tag
 CC gene comprising at least 5 20mer Tag sequences; a Poly A site having at
 CC least 21 consecutive A residues; a second restriction endonuclease site
 CC which may be the same or different than the first restriction
 CC endonuclease site; or a T7 promoter on the opposite strand as the T3
 CC promoter. The invention may be useful in nucleic acid analysis, in
 CC particular to synthetic Tag genes useful as assay controls, in assay
 CC development, product development and validation and for quality control.
 CC The present sequence is that of a Tag oligonucleotide probe which may be
 CC used during the creation of the novel DNA molecule of the invention.
 XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 61.0%; Score 12.8; DB 12; Length 20;
 Best Local Similarity 87.5%; Pred. No. 1.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GCGTATCTCGAGAGTC 19
 Db 17 GCGTATCTCGCATAGTC 2
 RESULT 10
 ID ADK96254
 XX ADK96254 standard; DNA; 20 BP.
 AC ADK96254;
 XX 06-MAY-2004 (first entry)
 DT Primer of the invention #1974.
 XX human; single nucleotide polymorphism; SNP; ss; primer.
 OS Synthetic.
 XX JP2003259875-A.
 XX 16-SEP-2003.
 XX 08-MAR-2002; 2002JP-00064373.
 XX 08-MAR-2002; 2002JP-00064373.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2004-093977/10.
 XX Novel polynucleotide useful for PCR amplification along with two DNA
 PT fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.
 XX Claim 2; SEQ ID NO 5283; 2627pp; Japanese.
 PS The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.

```
SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 12; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGTATCTGAAGA 16
DB 3 CTGGCATAGCTGAAGA 18

RESULT 11
ADF50105
ID ADF50105 standard; RNA; 21 BP.
XX
AC ADF50105;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human BCL2 siRNA target sequence SEQ ID NO:833.
XX
KW ss; siRNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytosstatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
OS Homo sapiens.
XX
PN WO2003070969-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-US004908.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L;
XX
WPI; 2003-712622/67.
XX
New short interfering nucleic acid, useful e.g. for treatment and
diagnosis of cancer or autoimmune disease, downregulates expression of
the BCL2 gene.
XX
Example 3; SEQ ID NO 833; 148pp; English.
XX
The invention relates to a novel short interfering nucleic acid (siRNA)
that downregulates expression of the BCL2 gene by RNA interference. A
siRNA of the invention has cytostatic, immunosuppressive, virucide, and
anti-HIV activity. The siRNA are useful for modulation (inhibition) of
expression or activity of BCL2 by RNA interference. siRNA are used to
modulate expression of BCL2 genes, in cells, tissue explants or
organisms, e.g. for treating cancer, autoimmune diseases and viral
infections (including by HIV) but also for drug screening, diagnosis,
target identification and validation, genetic engineering, (e.g. of single
pharmacogenomics, studying gene function and gene mapping, (e.g. of single
nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
represent siRNA of the invention.
XX
SQ Sequence 21 BP; 3 A; 5 C; 5 G; 2 T; 6 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 56.2%; Pred. No. 1.4e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

SQ Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTATCTGAAGAGTCTG 21
DB 16 GTCTCTGAAGACTCTG 1

RESULT 13
```

```
ADF50125/C
ID ADF50125 standard; RNA; 21 BP.
XX
AC ADF50125;
XX
XX 12-FEB-2004 (first entry)
DT
DE Human BCL2 siNA target sequence SEQ ID NO:853.
XX
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
OS
XX WO2003070969-A2.
PN
XX 28-AUG-2003.
PD
XX 18-FEB-2003; 2003WO-US004908.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX 18-JUL-2002; 2002US-0396905P.
PR
XX 29-AUG-2002; 2002US-0406784P.
PR
XX 05-SEP-2002; 2002US-0408378P.
PR
XX 09-SEP-2002; 2002US-0409293P.
PR
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Beigelman L;
PI
XX WPI; 2003-712622/67.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
XX Example 3; SEQ ID NO 853; 148pp; English.
PS
XX The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADP50143
CC represent siNA of the invention.
XX
XX Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;
SQ
Query Match 61.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTATCTGAAGAGTCTG 21
DB 16 GTCTCTGAAGAGTCTG 1

RESULT 14
ADF50109/C
ID ADF50109 standard; RNA; 21 BP.
XX
XX ADF50109;
AC
XX 12-FEB-2004 (first entry)
DT
```

```
XX
DE Human BCL2 siNA target sequence SEQ ID NO:837.
XX
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
OS
XX WO2003070969-A2.
PN
XX 28-AUG-2003.
PD
XX 18-FEB-2003; 2003WO-US004908.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX 18-JUL-2002; 2002US-0396905P.
PR
XX 29-AUG-2002; 2002US-0406784P.
PR
XX 05-SEP-2002; 2002US-0408378P.
PR
XX 09-SEP-2002; 2002US-0409293P.
PR
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Mcswiggen J, Beigelman L;
PI
XX WPI; 2003-712622/67.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
XX Example 3; SEQ ID NO 837; 148pp; English.
PS
XX The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADP50143
CC represent siNA of the invention.
XX
XX Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;
SQ
Query Match 61.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTATCTGAAGAGTCTG 21
DB 16 GTCTCTGAAGAGTCTG 1

RESULT 15
ADG29696
ID ADG29696 standard; RNA; 21 BP.
XX
XX AC ADG29696;
XX
XX 26-FEB-2004 (first entry)
DT
XX BCL2-targeted siNA DNA-RNA hybrid - SEQ ID 262.
XX
XX double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
```


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OM nucleic - nucleic search, using sw model
Run on: June 8, 2006, 21:45:36 ; Search time 290 Seconds
(without alignments)
528.929 Million cell updates/sec

Title: US-09-743-825-7
Perfect score: 22
Sequence: 1 gcattacagtagaagcc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 3139352

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 8:
1: Geneseqn1980s:
2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002as:
7: Geneseqn2002bs:
8: Geneseqn2003as:
9: Geneseqn2003bs:
10: Geneseqn2003cs:
11: Geneseqn2003ds:
12: Geneseqn2004as:
13: Geneseqn2004bs:
14: Geneseqn2005s:
15: Geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAZ50444	AAZ50444 EST R0050
2	15.2	69.1	20	AAZ50444	AAZ50444 EST R0050
3	13.2	60.0	21	AAI198006	AAI198006 Lawsonia
4	13.2	60.0	21	ACA92364	ACA92364 Lawsonia
5	13.2	60.0	21	ADG33930	ADG33930 L. intrac
6	13.2	60.0	21	ADJ66835	ADJ66835 Lawsonia
7	13.2	60.0	21	ADR72987	ADR72987 Lawsonia
8	13.2	60.0	21	ABE18062	ABE18062 L. intrac
9	13	59.1	22	AAF85459	AAF85459 Polynucle
10	12.8	58.2	18	AEC52046	AEC52046 Antisense
11	12.8	58.2	18	AEC51906	AEC51906 Antisense
12	12.8	58.2	18	AEC51766	AEC51766 Antisense
13	12.8	58.2	19	AAA60336	AAA60336 Human HPC
14	12.8	58.2	19	AAI99071	AAI99071 Human pro
15	12.8	58.2	20	AAT33010	AAT33010 Mouse SRY
16	12.8	58.2	20	ABK87666	ABK87666 Synthetic
17	12.8	58.2	20	ADA66516	ADA66516 Transform
18	12.8	58.2	21	ADG89282	ADG89282 Cancer de

c 19	12.8	58.2	21	12	ADP27751	Adp27751 PCR prime
c 20	12.8	58.2	21	13	ADR00153	Adr00153 COX2 prob
c 21	12.8	58.2	21	14	ADM45702	Adm45702 Reverse R
c 22	12.8	58.2	21	14	ADW72150	Adw72150 Reverse P
c 23	12.6	57.3	19	14	ADW73436	Adw73436 Human B7-
c 24	12.6	57.3	19	14	ADW73461	Adw73461 Human B7-
c 25	12.6	57.3	20	12	ADQ13916	Adq13916 DMD regio
c 26	12.6	57.3	20	14	ADX03606	Adx03606 Antisense
c 27	12.6	57.3	20	14	ADY98387	Ady98387 eIF4E ant
c 28	12.6	57.3	20	14	ADY98415	Ady98415 Eukaryoti
c 29	12.6	57.3	20	14	ADY98302	Ady98302 eIF4E ant
c 30	12.6	57.3	20	14	ADY98416	Ady98416 Eukaryoti
c 31	12.4	56.4	19	14	ADY03829	Ady03829 Human cor
c 32	12.4	56.4	19	14	AEA34557	Aea34557 Human TRP
c 33	12.4	56.4	19	14	AEA44481	Aea44481 Human TRP
c 34	12.4	56.4	20	10	ADD18145	Adi18145 Human G-p
c 35	12.4	56.4	20	12	ADI41032	Adi41032 Human HGP
c 36	12.4	56.4	21	10	ABT16558	Abt16558 Ethylene
c 37	12.2	55.5	18	2	AAQ61732	Aaq61732 HEV strai
c 38	12.2	55.5	18	2	AAI27443	Aai27443 HEV strai
c 39	12.2	55.5	18	2	AAV71653	Aav71653 HEV ORF p
c 40	12.2	55.5	18	3	AAZ70423	Aaz70423 Human bia
c 41	12.2	55.5	20	6	ABN89231	Abn89231 Human Tal
c 42	12.2	55.5	20	6	ADG90494	Adg90494 Human tal
c 43	12.2	55.5	20	10	ADC65754	Adc65754 Human TGP
c 44	12.2	55.5	20	10	ADF90932	Adf90932 Microorga
c 45	12.2	55.5	20	10	ABZ86479	Abz86479 Human oli

ALIGNMENTS

RESULT 1
AAZ50444
ID AAZ50444 standard; DNA; 22 BP.

XX AC AAZ50444;

XX DT 18-MAY-2000 (first entry)

XX DE EST R00504-specific primer 1.

XX KW PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer;
XX KW prostate epithelium; splicing mechanism; early diagnosis; progression;
XX KW precancerous cell; metastatic potential; non-neoplastic prostate disease;
XX KW expressed sequence tag; EST; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200005376-A1.

XX PD 03-FEB-2000.

XX PF 23-JUL-1999; 99WO-US016831.

XX PR 24-JUL-1998; 98US-0094137P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Chuaqui RF, Cole KA, Liotta LA;

XX DR WPI; 2000-182700/16.

XX Novel gene which is dysregulated in prostate cancer useful for diagnosing cancer.

XX PS Claim 5; Page 16; 51pp; English.

XX The present sequence is the EST AAR00504-specific PCR primer, used for
XX amplification of sequences contained within the EST AAR00504. It is
XX useful to probe the gene overexpressed in prostate cancer epithelium and
XX to analyse the differential expression of the EST. The PB39 gene that is
XX dysregulated in prostate cancer is isolated from human pancreas cDNA

CC library and has homology to the EST AAR00504. PB39 gene is located on
 CC chromosome lip11.1-11.2. Abnormally high concentrations of PB39 are found
 CC in prostate tissue derived from prostate cancer (PC) epithelium. PB39
 CC sequence is useful for detection of precancerous or cancer cells in the
 CC prostate. PB39 is useful for early diagnosis of the progression of
 CC prostate cancer, especially in aggressive prostate carcinoma. It can also
 CC distinguish PC from other non-neoplastic prostate disease. The diagnostic
 CC method is selective and specific for various types of PC and also
 CC facilitates identifying prostate cancer of differing aggressiveness and
 CC metastatic potential
 XX
 SQ Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0;

Qy 1 GCATGTTACAGGTAGAAAAGCC 22
 |||||
 Db 1 GCATGTTACAGGTAGAAAAGCC 22

RESULT 2

AA956007/C
 ID AAX96007 standard; DNA; 20 BP.
 XX
 AC AAX96007;

DT 13-SEP-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.

XX Synthetic.

OS Chlamydia pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GSEST) GENSET.

XX Griffais R;

XX WPI, 1999-357842/30.

PT Genome sequence of Chlamydia pneumoniae.

PS Page 1792; Disclosure; 1912pp; English.

CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAX34584- AAX35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 69.1%; Score 15.2; DB 2; Length 20;

Best Local Similarity 85.0%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGGTAGAAAAG 20
 |||||
 Db 20 GCCTGTTCCAGATAGAAAAG 1

RESULT 3

AAI98006

ID AAI98006 standard; DNA; 21 BP.

XX
 AC AAI98006;

DT 20-NOV-2001 (first entry)

XX Lawsonia intracellularis protein related oligonucleotide SEQ ID NO: 50.

XX HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
 KW vaccine; PCR primer; probe; ss.

XX Lawsonia intracellularis.

XX JP2001169787-A.

XX 26-JUN-2001.

XX 20-OCT-2000; 2000JP-00320736.

XX 22-OCT-1999; 99US-0160922P.

XX (PFIZ) PFIZER PROD INC.

XX WPI; 2001-592540/67.

XX Lawsonia intracellularis polynucleotide and encoded protein, used to
 PT prevent Lawsonia intracellularis infection.

XX Example 2; Page 55; 67pp; Japanese.

XX The present invention provides isolated polynucleotides encoding HtrA,
 CC PonA, HypC, Lyss, YefW, ABC1 or Omp100 protein of Lawsonia
 CC intracellularis. The sequences can be used in vaccines for the prevention
 CC of Lawsonia intracellularis infection. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention

XX Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 4; Length 21;

Best Local Similarity 83.3%; Pred. No. 1.4e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTCACAGGTAGAAAAGC 21

|||

Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 4

ACA92364

ID ACA92364 standard; DNA; 21 BP.

XX
 AC ACA92364;

DT 16-JUL-2003 (first entry)

XX Lawsonia intracellularis DNA PCR primer #41.

XX Primer; ss; antibacterial; HtrA; PonA; HypC; Lyss; YcfW; ABC1; Omp100;
 KW Lawsonia intracellularis infection; Orf1; pgi; PCR.

XX Lawsonia intracellularis.

XX US2003021802-A1.

```

XX PD 30-JAN-2003.
XX PR
XX PF 01-AUG-2002; 2002US-00210296.
XX PP
XX PR 22-OCT-1999; 99US-0160922P.
XX PR 05-NOV-1999; 99US-0163858P.
XX PR 12-OCT-2000; 2000US-00689065.
XX PR
XX PA (ROSE/) ROSEY E L.
XX PI
XX PI Rosey EL;
XX DR WPI; 2003-416977/39.
XX DR
XX PT New isolated Lawsonia intracellularis polynucleotide and polypeptide,
XX PT useful for the prevention and diagnosis of Lawsonia infections in
XX PT susceptible animals, such as pigs.
XX PS Example 2; Page 46; 64pp; English.
XX CC The invention relates to an isolated polynucleotide molecule comprising a
XX CC sequence encoding Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW,
XX CC ABC1 or Omp100 protein. The invention also relates to a genetic construct
XX CC comprising a polynucleotide molecule that can be used to alter a Lawsonia
XX CC gene, comprising a polynucleotide molecule comprising a sequence that is
XX CC otherwise the same as a nucleotide sequence of a htrA, ponA, hypC, lysS,
XX CC ycfW, abc1 or omp100 gene, or its homologue, a substantial portion, or
XX CC mutations capable of altering the above mentioned genes or a
XX CC polynucleotide molecule comprising a sequence that naturally flanks in
XX CC situ the ORF of the htrA, ponA, hypC, lysS, ycfW, abc1 or omp100 gene or
XX CC its homologue. The invention also relates to a fusion protein of a
XX CC polypeptide of the invention fused to another polypeptide or an analogue
XX CC or derivative. The invention further relates to a substantially pure
XX CC polypeptide comprising an epitope of HtrA, PonA, HypC, LysS, YcfW, ABC1
XX CC or Omp100 protein that is specifically reactive with anti-Lawsonia
XX CC antibodies. The methods and compositions of the present invention are
XX CC useful for the prevention and diagnosis of L. intracellularis infections
XX CC in susceptible animals, such as pigs. Sequences ACA92324-ACA92415
XX CC represent PCR primers used to amplify DNA encoding L. intracellularis
XX CC proteins of the invention
XX SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 9; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTTACAGGTAGAAAAGC 21
Db ||||| ||||| |||||
2 TGGTACAGCAAGAAAAGC 19

RESULT 5
ADG33930
ID ADG33930 standard; DNA; 21 BP.
AC ADG33930;
XX XX
XX DT 26-FEB-2004 (first entry)
XX DE L. intracellularis sequencing primer #26.
XX KW Lawsonia intracellularis; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100;
XX KW pig; ss; sequencing; primer.
XX OS Lawsonia intracellularis.
XX XX
XX PN US2003202983-A1.
XX XX
XX PD 30-OCT-2003.
XX PS 29-MAY-2003; 2003US-00449462.

```

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XX PR 22-OCT-1999; 99US-0160922P.
XX PR 05-NOV-1999; 99US-0163858P.
XX PR 12-OCT-2000; 2000US-00689065.
XX PR
XX PA (ROSE/) ROSEY E L.
XX PI
XX PI Rosey EL;
XX DR WPI; 2003-900619/82.
XX DR
XX PT New isolated Lawsonia intracellularis polynucleotide and polypeptide,
XX PT useful for the prevention and diagnosis of Lawsonia infections in
XX PT susceptible animals, such as pigs.
XX PS Example 2; SEQ ID NO 50; 66pp; English.
XX CC The invention relates to a new isolated polynucleotide molecule which
XX CC encodes Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1 or
XX CC Omp100 protein. The methods and compositions of the present invention are
XX CC useful for the prevention and diagnosis of L. intracellularis infections
XX CC in susceptible animals, such as pigs. The present sequence is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTTACAGGTAGAAAAGC 21
Db ||||| ||||| |||||
2 TGGTACAGCAAGAAAAGC 19

RESULT 6
ADJ66835
ID ADJ66835 standard; DNA; 21 BP.
XX AC ADJ66835;
XX DT 06-MAY-2004 (first entry)
XX DE Lawsonia intracellularis PCR primer SeqID50.
XX KW antibacterial; vaccine; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100;
XX KW diagnostic agent; infection; pig; porcine proliferative enteropathy; PCR;
XX KW primer; ss.
XX OS Lawsonia intracellularis.
XX PN US6605696-B1.
XX PD 12-AUG-2003.
XX PF 12-OCT-2000; 2000US-00689065.
XX PR 22-OCT-1999; 99US-0160922P.
XX PR 05-NOV-1999; 99US-0163858P.
XX PA (PFIZ ) PFIZER INC.
XX PA (PFIZ ) PFIZER PROD INC.
XX PI
XX PI Rosey EL;
XX DR WPI; 2003-895290/82.
XX DE New Lawsonia intracellularis polypeptides, useful as vaccines, as
XX DE diagnostic agents, or in preventing infections in susceptible animals
XX DE such as pigs, e.g. porcine proliferative enteropathy.
XX PS Example 2; SEQ ID NO 50; 62pp; English.

```

CC This invention relates to a novel isolated polypeptide derived from
 CC Lawsonia intracellularis. The invention may be useful for the development
 CC of compounds with an antibacterial activity or a vaccine. Specifically
 CC claimed are L intracellularis proteins, such as HtrA, PonA, HypC, Lyss,
 CC YcfW, ABC1 and Omp100 proteins. The invention may be useful for the
 CC development of vaccines, diagnostic agents, or in preventing L
 CC intracellularis infections in susceptible animals such as pigs, for
 CC example porcine proliferative enteropathy. The present sequence is that
 CC of a PCR primer which was used for amplification and/or sequencing of a
 CC region of L intracellularis DNA during the exemplification of the
 CC invention.

XX
 SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 10; Length 21;
 Best Local Similarity 83.3%; Pred. No. 1.4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGGTACAGGTAGAAAAGC 21
 |||||
 Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 7

ADR72987

ID ADR72987 standard; DNA; 21 BP.

XX

AC ADR72987;

XX

DT 04-NOV-2004 (first entry)

XX

DE Lawsonia intracellularis DNA sequence #41.

XX

KW HtrA; PonA; HypC; Lyss; YcfW; ABC1; Omp100; infection; primer; probe; ss.

XX

OS Lawsonia intracellularis.

XX

PN JP2004229667-A.

XX

PD 19-AUG-2004.

XX

PF 26-MAR-2004; 2004JP-00092095.

XX

PR 22-OCT-1999; 99US-0160922P.

XX

PR 20-OCT-2000; 2000JP-00320736.

XX

PA (PFIZ) PFIZER PROD INC.

XX

DR WPI; 2004-597336/58.

XX

PT Novel isolated polynucleotide comprising Lawsonia intracellularis

PT nucleotide sequence that encodes HtrA, PonA, HypC, Lyss, YcfW, ABC1 or

PT Omp100 protein or its essential portion, useful as diagnostic agent.

XX

FS Example 2; SEQ ID NO 50; 55pp; Japanese.

XX

CC The invention comprises the amino acid and coding sequences of the
 CC Lawsonia intracellularis proteins: HtrA, PonA, HypC, Lyss, YcfW, ABC1,
 CC and Omp100. The DNA and protein sequences of the invention are useful for
 CC preventing Lawsonia intracellularis infection of animals (e.g. pig). The
 CC present DNA sequence was used in the exemplification of the invention.
 CC NOTE: The present sequence is not shown in the specification but was
 CC obtained from the Japanese Patent Office.

XX

SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 13; Length 21;
 Best Local Similarity 83.3%; Pred. No. 1.4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGGTACAGGTAGAAAAGC 21
 |||||
 Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 8

ABE18062

ID ABE18062 standard; DNA; 21 BP.

XX

AC ABE18062;

XX

DT 08-SEP-2005 (first entry)

XX

DE L. intracellularis gene cluster B sequencing primer, ER178, SEQ: 50.

XX

KW Diagnosis; vaccine; infection; antimicrobial; enteropathy;

KW gastrointestinal-gen.; gastrointestinal disease; HtrA; PonA; HypC; Orf1;

XX primer; ss.

OS Lawsonia intracellularis.

XX

PN US2005143561-A1.

XX

PD 30-JUN-2005.

XX

PF 30-MAY-2003; 2003US-00449648.

XX

PR 22-OCT-1999; 99US-0160922P.

XX

PR 05-NOV-1999; 99US-0163858P.

XX

PR 12-OCT-2000; 2000US-00689065.

XX

PA (ROSE/) ROSEY E L.

XX

FI Rosey EL;

XX

DR WPI; 2005-457804/46.

XX

PT New isolated Lawsonia intracellularis HypC proteins useful for diagnosing

PT or preventing infections caused by L. intracellularis in susceptible

PT animals, such as pigs.

XX

PS Example 2; SEQ ID NO 50; 65pp; English.

XX

CC The invention relates to Lawsonia intracellularis HypC protein and a
 CC nucleotide sequence that encodes L. intracellularis HtrA, PonA, HypC,
 CC Lyss, YcfW, ABC1, orf1 and Omp100 protein. The invention also relates to
 CC an immunogenic composition or vaccine comprising an immunogenic amount of
 CC the proteins of the invention in combination with a pharmaceutical
 CC carrier. The composition is useful for diagnosing or preventing

CC infections caused by L. intracellularis porcine proliferative enteropathy

CC (PPE) in susceptible animals such as pigs. The present sequence is a

CC primer used for sequencing pER392 Lawsonia intracellularis gene cluster B

CC containing HtrA, PonA, HypC and Orf1 genes.

XX

SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 14; Length 21;
 Best Local Similarity 83.3%; Pred. No. 1.4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGGTACAGGTAGAAAAGC 21
 |||||
 Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 9

AAF85459/C

ID AAF85459 standard; DNA; 22 BP.

XX

AC AAF85459;

XX

DT 23-JUL-2001 (first entry)

XX

DE Polynucleotide in unique region in exon 1 of rabbit motilin receptor.

XX

KW Motilin receptor; gastrointestinal disease; gastric motility disorder;

KW gastroparesis; irritable bowel syndrome; diarrhoea; ss.
 XX Oryctolagus cuniculus.
 XX WO200132710-A1.
 XX 10-MAY-2001.
 XX 25-OCT-2000; 2000WO-US029426.
 XX 29-OCT-1999; 99US-0162264P.
 XX (MERI) MERCK & CO INC.
 XX Tan C, McKee K;
 XX WPI; 2001-343479/36.
 XX Novel polypeptides related to dog and rabbit motilin receptor
 PT polypeptide, comprising unique regions from dog and motilin receptor
 PT amino acid sequence, useful for identifying compounds for treating
 PT diarrhea in humans.
 XX Claim 17; Page 22; 42pp; English.
 XX AAP85456-60 represent polynucleotide sequences from the unique region of
 CC exon 1 of a rabbit motilin receptor gene. The specification describes an
 CC unique sequence present in exon 1 of the motilin receptor, which is not
 CC present in human or Sphaeroides naphelus 7587 motilin receptor sequences.
 CC The unique nucleic acid sequence is useful for measuring the ability of a
 CC compound to affect motilin receptor activity. Motilin receptor
 CC polynucleotides and polypeptides are used to identify therapeutic
 CC compounds which are useful for treating gastrointestinal diseases and
 CC disorders such as gastric motility disorders, gastroparesis, irritable
 CC bowel syndrome, and diarrhoea
 XX Sequence 22 BP; 2 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 59.1%; Score 13; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 9 CAGGTAGAAAAGC 21
 Db |||||
 13 CAGGTAGAAAAGC 1
 RESULT 10
 AEC52046/c
 ID AEC52046 standard; DNA; 18 BP.
 XX AEC52046;
 AC AEC52046;
 XX 17-NOV-2005 (first entry)
 XX Antisense oligonucleotide targeting human TGF-beta-3 #444.
 XX Transforming growth factor beta; TGF-beta-3; antisense therapy;
 KW antisense oligonucleotide; ss; cancer; cytostatic.
 XX Homo sapiens.
 XX WO2005084712-A2.
 XX 15-SEP-2005.
 XX 28-FEB-2005; 2005WO-EP002101.
 XX 27-FEB-2004; 2004EP-00004478.
 XX 01-APR-2004; 2004US-0558135P.
 XX (ANTI-) ANTISENSE PHARMA GMBH.
 XX

PI Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;
 PI Bischof A, Hafner M, Egger T,
 XX WPI; 2005-630685/64.
 XX New antisense oligonucleotides inhibiting the synthesis of proteins
 PT involved in the formation of metastases such as transforming growth
 PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
 PT treating cancer.
 XX Claim 4; Page 71; 106pp; English.
 XX The invention relates to an antisense oligonucleotide or its active
 CC derivative selected from AEC46374-AEC46395, targeting human interleukin-
 CC 10 (IL-10). Also included are a process of manufacturing the antisense
 CC oligonucleotide (or its active derivative, by adding consecutive
 CC nucleosides and linker stepwise or by cutting the oligonucleotide out of
 CC longer oligonucleotide chain), a pharmaceutical composition comprising
 CC the antisense oligonucleotide and a TGF-beta 2 antagonist for preparing a
 CC composition for treating cancer. The oligonucleotide is an antisense
 CC oligonucleotide inhibiting the synthesis of proteins involved in the
 CC formation of metastases. The oligonucleotide is an antisense
 CC oligonucleotide inhibiting the production of transforming growth factor
 CC (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules
 CC (CAMs), integrins, selectins, metalloproteases (MMPs), their tissue
 CC inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are
 CC useful for the preparation of a pharmaceutical composition for inhibiting
 CC the formation of metastases in cancer treatment. The oligonucleotides are
 CC useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,
 CC brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the
 CC kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical
 CC carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,
 CC endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder
 CC cancer, gastric cancer, head and neck cancer, hepatocellular cancer,
 CC liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell
 CC bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma,
 CC papillary carcinoma, papillary adenocarcinoma, prostate cancer, small
 CC intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland
 CC carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,
 CC testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,
 CC trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
 CC Ewing's tumor, craniopharyngioma, ependymoma, medulloblastoma,
 CC hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma,
 CC neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,
 CC Wilm's tumor and/or myeloma, multiple. The present sequence is an
 CC antisense oligonucleotide targeting human TGF-beta-3.
 XX Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 58.2%; Score 12.8; DB 14; Length 18;
 Best Local Similarity 87.5%; Pred. No. 2.2e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 7 TACAGGTAGAAAGCC 22
 Db |||||
 16 TACAGGTAGAAATCC 1
 RESULT 11
 AEC51906/c
 ID AEC51906 standard; DNA; 18 BP.
 XX AEC51906;
 AC AEC51906;
 XX 17-NOV-2005 (first entry)
 XX Antisense oligonucleotide targeting human TGF-beta-3 #304.
 XX Transforming growth factor beta; TGF-beta-3; antisense therapy;
 KW antisense oligonucleotide; ss; cancer; cytostatic.
 XX Homo sapiens.
 XX

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PN WO2005084712-A2.
XX 15-SEP-2005.
XX 28-FEB-2005; 2005WO-EP002101.
XX 27-FEB-2004; 2004EP-00004478.
PR 01-APR-2004; 2004US-0558135P.
XX (ANTI-) ANTISENSE PHARMA GMBH.
PA
XX Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;
PI Bischof A, Hafner M, Egger T;
XX WPI; 2005-630685/64.
DR
XX New antisense oligonucleotides inhibiting the synthesis of proteins
PT involved in the formation of metastases such as transforming growth
PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
PT treating cancer.
XX
XX Claim 4; Page 70; 106pp; English.
XX
XX The invention relates to an antisense oligonucleotide or its active
XX derivative selected from AEC46374-AEC46395, targeting human interleukin-
XX 10 (IL-10). Also included are a process of manufacturing the antisense
XX oligonucleotide (or its active derivative, by adding consecutive
XX nucleosides and linker stepwise or by cutting the oligonucleotide out of
XX longer oligonucleotide chain), a pharmaceutical composition comprising
XX the antisense oligonucleotide and a TGF-beta 2 antagonist for preparing a
XX composition for treating cancer. The oligonucleotide is an antisense
XX oligonucleotide inhibiting the synthesis of proteins involved in the
XX formation of metastases. The oligonucleotide is an antisense
XX oligonucleotide inhibiting the production of transforming growth factor
XX (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules
XX (CAMS), integrins, selectins, metalloproteases (MMPs), their tissue
XX inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are
XX useful for the preparation of a pharmaceutical composition for inhibiting
XX the formation of metastases in cancer treatment. The oligonucleotides are
XX useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,
XX brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the
XX kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical
XX carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,
XX endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder
XX cancer, gastric cancer, head and neck cancer, hepatocellular cancer,
XX liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell
XX bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma,
XX papillary carcinoma, papillary adenocarcinoma, prostate cancer, small
XX intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland
XX carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,
XX testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,
XX trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
XX Ewing's tumor, craniopharyngioma, ependymoma, medulloblastoma,
XX hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma,
XX neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,
XX Wilm's tumor and/or myeloma, multiple. The present sequence is an
XX antisense oligonucleotide targeting human TGF-beta-3.
XX
XX Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
SQ
Query Match 58.2%; Score 12.8; DB 14; Length 18;
Best Local Similarity 87.5%; Pred. NO. 2.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 TACAGGTAGAAAAGCC 22
DB 17 TACAGGGGAGAAATCC 2
RESULT 12
AEC51766/c
ID AEC51766 standard; DNA; 18 BP.
XX

```

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AC AEC51766;
XX 17-NOV-2005 (first entry)
XX DE Antisense oligonucleotide targeting human TGF-beta-3 #164.
XX XX Transforming growth factor beta; TGF-beta-3; antisense therapy;
KW antisense oligonucleotide; ss; cancer; cytostatic.
XX OS Homo sapiens.
XX PN WO2005084712-A2.
XX PD 15-SEP-2005.
XX PF 28-FEB-2005; 2005WO-EP002101.
XX PR 27-FEB-2004; 2004EP-00004478.
PR 01-APR-2004; 2004US-0558135P.
XX (ANTI-) ANTISENSE PHARMA GMBH.
XX PI Schlingensiepen K, Schlingensiepen R, Jachimczak P, Stauder G;
PI Bischof A, Hafner M, Egger T;
XX WPI; 2005-630685/64.
DR
XX New antisense oligonucleotides inhibiting the synthesis of proteins
PT involved in the formation of metastases such as transforming growth
PT factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
PT treating cancer.
XX
XX Claim 4; Page 70; 106pp; English.
XX
XX The invention relates to an antisense oligonucleotide or its active
XX derivative selected from AEC46374-AEC46395, targeting human interleukin-
XX 10 (IL-10). Also included are a process of manufacturing the antisense
XX oligonucleotide (or its active derivative, by adding consecutive
XX nucleosides and linker stepwise or by cutting the oligonucleotide out of
XX longer oligonucleotide chain), a pharmaceutical composition comprising
XX the antisense oligonucleotide and a TGF-beta 2 antagonist for preparing a
XX composition for treating cancer. The oligonucleotide is an antisense
XX oligonucleotide inhibiting the synthesis of proteins involved in the
XX formation of metastases. The oligonucleotide is an antisense
XX oligonucleotide inhibiting the production of transforming growth factor
XX (TGF)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules
XX (CAMS), integrins, selectins, metalloproteases (MMPs), their tissue
XX inhibitors (TIMPs) and/or interleukins 10. The oligonucleotides are
XX useful for the preparation of a pharmaceutical composition for inhibiting
XX the formation of metastases in cancer treatment. The oligonucleotides are
XX useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma,
XX brain tumor, breast cancer, bronchogenic carcinoma, carcinoma of the
XX kidney, cervical cancer, choriocarcinoma, cystadenocarcinoma, cervical
XX carcinoma, colon carcinoma, colorectal carcinoma, embryonal carcinoma,
XX endometrial cancer, epithelial carcinoma, esophageal cancer, gall bladder
XX cancer, gastric cancer, head and neck cancer, hepatocellular cancer,
XX liver carcinoma, lung carcinoma, medullary carcinoma, non-small cell
XX bronchogenic/lung carcinoma, ovarian cancer, pancreas carcinoma,
XX papillary carcinoma, papillary adenocarcinoma, prostate cancer, small
XX intestine carcinoma, rectal cancer, renal cell carcinoma, sebaceous gland
XX carcinoma, skin cancer, soft tissue cancer, squamous cell carcinoma,
XX testicular carcinoma, uterine cancer, acoustic neuromas, neurofibromas,
XX trachomas, and pyogenic granulomas; pre-malignant tumors, blastoma,
XX Ewing's tumor, craniopharyngioma, ependymoma, medulloblastoma,
XX hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma,
XX neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas,
XX Wilm's tumor and/or myeloma, multiple. The present sequence is an
XX antisense oligonucleotide targeting human TGF-beta-3.
XX
XX Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 58.2%; Score 12.8; DB 14; Length 18;
Best Local Similarity 87.5%; Pred. NO. 2.2e+04;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 TACAGGTAGAAAAGCC 22
||||| ||||| ||
Db 18 TACAGGGAGAAATCC 3

RESULT 13
AAA60336/c
ID AAA60336 standard; DNA; 19 BP.
XX
AC AAA60336;
XX
DT 07-DEC-2000 (first entry)
XX
DE Human HPC2 cDNA exon 18 mutation screening primer SEQ ID NO: 157.
XX
KW Human; mouse; prostate cancer predisposing gene; HPC2;
KW human chromosome 17p; gene therapy; peptide therapy; drug design;
KW PCR primer; sequencing primer; ss.
XX
OS Homo sapiens.
XX
FN WO200027864-A1.
XX
PD 18-MAY-2000.
XX
PP 05-NOV-1999; 99WO-US026055.
XX
XX 06-NOV-1998; 98US-0107468P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX WPI; 2000-376481/32.
DR
XX Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies,
XX useful for treatment and diagnosis of prostate cancer.
PT
XX Example 5; Page 61; 157pp; English.
XX
CC The present sequence is a primer used in the isolation of the human and
CC murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC version of the gene is found on chromosome 17p. Some alleles cause a
CC predisposition to cancer, particularly prostate cancer. This gene and its
CC protein can be used in peptide and gene therapy for cancer patients, as
CC well as being useful as diagnostic tools (both for cancer sufferers and
CC those with a predisposition to the disease) and in the production of
CC cancer drugs
XX
SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 58.2%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ATGTTACAGGTAGAAA 18
||||| ||||| |||||
Db 19 ATGTCACAGGCAGAAA 4

RESULT 14
AAS99071/c
ID AAS99071 standard; DNA; 19 BP.
XX
AC AAS99071;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human prostate cancer predisposing gene (HPC2) PCR primer #67.
XX
KW Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;

KW gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
KW sequencing primer; PCR primer.
OS Homo sapiens.
XX
PN WO200185911-A2.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014602.
XX
PR 05-MAY-2000; 2000US-00564805.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX WPI; 2002-066599/09.
DR
XX Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
PT for prostate cancer, is useful in gene therapy techniques to restore HPC2
PT normal levels by which neoplastic growth is suppressed in recipient cell.
XX
PS Example 8; Page 74; 239pp; English.
XX
CC The invention relates to a human prostate cancer predisposing gene coding
CC for an HPC2 polypeptide. The DNA and protein sequences are useful as
CC diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in
CC a suspected mutant HPC2 allele by comparing the sequence of the suspected
CC mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also
CC useful for detecting an alteration in HPC2, where the alteration is
CC associated with cancer in a human. The method involves analysing an HPC2
CC gene or an HPC2 gene expression product from a tissue of the human. The
CC HPC2 gene is useful as a marker for prostate cancer and can be used in
CC gene therapy techniques to suppress neoplastic growth of recipient cells
CC which carry the mutant HPC2 allele. The sequences represent primers used
CC in the methods of the invention, cDNA encoding human and mouse HPC2 and
CC cDNA encoding HPC2 paralogues and orthologues
XX
SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 58.2%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ATGTTACAGGTAGAAA 18
||||| ||||| |||||
Db 19 ATGTCACAGGCAGAAA 4

RESULT 15
AAT33010/c
ID AAT33010 standard; DNA; 20 BP.
XX
AC AAT33010;
XX
DT 23-OCT-1996 (first entry)
XX
DE Mouse SRY-related gene primer 2.
XX
KW Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe;
KW HMG box; human; bovine; sex; animal; birth; ss.
XX
OS Synthetic.
XX
FN JP08154685-A.
XX
PD 18-JUN-1996.
XX
PF 30-NOV-1994; 94JP-00319525.
XX
PR 30-NOV-1994; 94JP-00319525.

XX (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.

XX WPI; 1996-336575/34.

XX Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex of
PT unborn animals.

XX Example 2; Page 6; 21pp; Japanese.

XX The primers AAT33009-10 were used to amplify a fragment of the gene
CC encoding a mouse SRY-related protein (AAT33007). This primer corresp. to
CC bases 7156-7175 of the mouse gene. The amplified fragment was used to
CC screen a mouse genomic library. The screen isolated 4 EcoRI fragments of
CC 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed a
CC 240 bp HMG box sequence between bases 7154-7393. Similarity with the
CC human SRY HMG box sequence resulted in primers being generated to amplify
CC the human SRY HMG box sequence for use as a probe to isolate the bovine
CC SRY-related gene (AAT33008). The mouse and bovine genes are useful for
CC determining the sex of an animal prior to birth

XX SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 58.2%; Score 12.8; DB 2; Length 20;

Best Local Similarity 87.5%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TACAGGTAGAAAGCC 22

Db 20 TCCAGGTGGAAGCC 5

Search completed: June 8, 2006, 21:51:02
Job time : 294 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 21:46:16 ; Search time 1977 Seconds
(without alignments)
711.605 Million cell updates/sec

Title: US-09-743-825-7

Perfect score: 22

Sequence: 1 gcattgtacagtagaagcc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1227620

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vl.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_on.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	15.2	69.1	20	2	AR314796	AR314796 Sequence
C 2	13.2	60.0	21	2	BD014939	BD014939 Lawsonia
C 3	13.2	60.0	21	2	AR374844	AR374844 Sequence
C 4	13.2	60.0	21	2	AX139516	AX139516 Sequence
C 5	12.8	58.2	19	2	BD231604	BD231604 Chromosome
C 6	12.8	58.2	19	2	AR631469	AR631469 Sequence
C 7	12.8	58.2	20	2	AR652656	AR652656 Sequence
C 8	12.8	58.2	20	2	AX405008	AX405008 Sequence
C 9	12.8	58.2	21	2	CQ876341	CQ876341 Sequence
C 10	12.8	58.2	21	2	CQ975123	CQ975123 Sequence
C 11	12.6	57.3	19	2	CS009834	CS009834 Sequence
C 12	12.6	57.3	19	2	CS009920	CS009920 Sequence
C 13	12.6	57.3	20	2	CS060643	CS060643 Sequence
C 14	12.6	57.3	20	2	CS060728	CS060728 Sequence
C 15	12.6	57.3	20	2	CS060757	CS060757 Sequence
C 16	12.6	57.3	20	2	CS060758	CS060758 Sequence
C 17	12.2	55.5	18	2	AR139875	AR139875 Sequence
C 18	12.2	55.5	18	2	AR167519	AR167519 Sequence

19	12.2	55.5	18	2	BD084547	BD084547 Recombina
20	12.2	55.5	18	2	AR234243	AR234243 Sequence
21	12.2	55.5	18	2	AR293044	AR293044 Sequence
22	12.2	55.5	18	2	AR476160	AR476160 Sequence
23	12.2	55.5	18	2	AR488045	AR488045 Sequence
24	12.2	55.5	18	2	AR579867	AR579867 Sequence
25	12.2	55.5	20	2	AR207150	AR207150 Sequence
26	12.2	55.5	20	2	AR271107	AR271107 Sequence
27	12.2	55.5	21	2	AX378485	AX378485 Sequence
28	12	54.5	20	2	AR118897	AR118897 Sequence
29	12	54.5	20	2	CQ763548	CQ763548 Sequence
30	12	54.5	20	2	AR297958	AR297958 Sequence
31	12	54.5	20	2	AX405002	AX405002 Sequence
32	12	54.5	21	2	AR575186	AR575186 Sequence
33	12	54.5	21	2	AX133296	AX133296 Sequence
34	12	54.5	21	8	AB213754	AB213754 Synthetic
35	12	54.5	22	2	CQ848304	CQ848304 Sequence
36	12	54.5	22	2	DD191176	DD191176 Method fo
37	11.8	53.6	17	2	BD063649	BD063649 Nucleotid
38	11.8	53.6	19	2	CS102002	CS102002 Sequence
39	11.8	53.6	19	2	CS102139	CS102139 Sequence
40	11.8	53.6	19	2	AR294337	AR294337 Sequence
41	11.8	53.6	20	2	A33496	A33496 Synthetic p
42	11.8	53.6	20	2	AR162418	AR162418 Sequence
43	11.8	53.6	20	2	I42395	I42395 Sequence 27
44	11.8	53.6	20	2	AX405006	AX405006 Sequence
45	11.8	53.6	20	2	AX405010	AX405010 Sequence

ALIGNMENTS

RESULT 1	AR314796/c	AR314796	Sequence 5333 from patent US 6559294.	20 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	AR314796	Sequence 5333 from patent US 6559294.					
ACCESSION	AR314796						
VERSION	AR314796.1	GI:31708222					
KEYWORDS	Source	Unknown.					
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 20)						
AUTHORS	Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.						
TITLE	Chlamydia pneumoniae polynucleotides and uses thereof						
JOURNAL	Patent: US 6559294-A 5333 06-MAY-2003;						
	Genset, S.A.;						
FEATURES	PRX;						
source	Location/Qualifiers						
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	/mol_type="genomic DNA"						
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Best Local Similarity	85.0%;	Pred. NO. 2.7e+04;					
Matches	17;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;		
Qy	1 GCATGTTACAGTAGAAG 20						
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RESULT 2							
BD014939	BD014939	21 bp	DNA	linear	PAT 27-AUG-2002		
LOCUS	Lawsonia intracellularis protein and methods and materials relating thereto.						
DEFINITION	BD014939						
ACCESSION	BD014939.1	GI:22555746					
VERSION	JP 2001169787-A/43.						
KEYWORDS	Lawsonia intracellularis						
SOURCE							

ORGANISM Lawsonia intracellularis
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Lawsonia.

REFERENCE 1 (bases 1 to 21)

AUTHORS Rosi, I. L.

TITLE Lawsonia intracellularis protein and methods and materials relating thereto

JOURNAL Patent: JP 2001159787-A 43 26-JUN-2001;

COMMENT OS Lawsonia intracellularis
PFIZER PRODUCTS INC
PN JP 2001169787-A/43
PD 26-JUN-2001
PF 20-OCT-2000 JP 2000320736
PR 22-OCT-1999 US 60/160922
PI IBURETTO LEE ROSI
PC C12N15/09,A61K38/00,A61K39/106,A61K48/00,A61P31/04,C07K14/205,
PC C07K16/12,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,G01N33/53,G01N33/569// PC
C12P21/02,
PC C12P21/08,(C12P21/02,C12R1:19),C12N15/00,A61K37/02,C12N5/00 CC
Lawsonia intracellularis protein and methods and materials CC
relating thereto

FH Key Location/Qualifiers

FT source 1..21

FEATURES source Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 83.3%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTCACGGTAGAAAAGC 21
||| ||||| ||||| |||||
Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 3

LOCUS AR374844
DEFINITION Sequence 50 from patent US 6605696.
ACCESSION AR374844
VERSION AR374844.1 GI:40077832
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)

AUTHORS Rosey, E.L.

TITLE Lawsonia intracellularis proteins, and related methods and materials

JOURNAL Patent: US 6605696-A 50 12-AUG-2003;
Pfizer, Inc. and Pfizer Products, Inc.; New York, NY

FEATURES source 1..21
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Query Match 60.0%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTCACGGTAGAAAAGC 21
||| ||||| ||||| |||||
Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 4

AX139516
LOCUS AX139516
DEFINITION Sequence 50 from Patent EP1094070.
ACCESSION AX139516
VERSION AX139516.1 GI:14275153
KEYWORDS
SOURCE
ORGANISM Lawsonia intracellularis
Lawsonia intracellularis
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Lawsonia.

REFERENCE 1

AUTHORS Rosey, E.L.

TITLE Lawsonia intracellularis proteins, and related methods and materials

JOURNAL Patent: EP 1094070-A 50 25-APR-2001;
Pfizer Products Inc. (US)

FEATURES source Location/Qualifiers
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/organism="Lawsonia intracellularis"
/mol_type="unassigned DNA"
/db_xref="taxon:29546"

ORIGIN

Query Match 60.0%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTCACGGTAGAAAAGC 21
||| ||||| ||||| |||||
Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 5

LOCUS BD231604/c
DEFINITION Chromosome 17q-linked prostate cancer susceptibility gene.
ACCESSION BD231604
VERSION BD231604.1 GI:33041374
KEYWORDS JP 2002529065-A/156.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS Tavtigian, S.V., Teng, D.H.F., Simard, J. and Rommens, J.M.

TITLE Chromosome 17q-linked prostate cancer susceptibility gene

JOURNAL Patent: JP 2002529065-A 156 10-SEP-2002;
MYRIAD GENETICS INC, THE HOSPITAL FOR SICK CHILDREN

COMMENT OS Homo sapiens (human)
PN JP 2002529065-A/156
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581041
PR 06-NOV-1998 US 60/107468
PI SEAN V TAVTIGIAN, DAVID H F TENG, JACQUES SIMARD, JOHANNA M PI ROWMENS
PC C12N15/09,A61K31/713,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P35/00,
PC C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12N5/10,
PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
PC G01N33/577,
PC G01N37/00,C12N15/00,A61K37/02,C12N5/00
CC Chromosome 17q-linked prostate cancer susceptibility gene FH
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FEATURES source Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

Query Match 58.2%; Score 12.8; DB 2; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATGTTACAGGTAGAAA 18
|||||
Db 19 ATGTCACAGGCAGAAA 4

RESULT 6

LOCUS AR631469/c 19 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 157 from patent US 6844189.
ACCESSION AR631469
VERSION AR631469.1 GI:59771253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Tavrigian,S.V., Teng,D.H.-F., Simard,J., Rommens,J.M., Cannon
Albright,L.A. and Neuhausen,S.B.
TITLE Chromosome 17p-linked prostate cancer susceptibility gene
JOURNAL Patent: US 6844189-A 157 18-JAN-2005;
Myriad Genetics, Inc.; University of Utah Research Foundation and
Hospital for Sick Children; Salt Lake City, UT
FEATURES
source
1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 58.2%; Score 12.8; DB 2; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATGTTACAGGTAGAAA 18
|||||
Db 19 ATGTCACAGGCAGAAA 4

RESULT 7

LOCUS AR652656/c 20 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 75 from patent US 6884787.
ACCESSION AR652656
VERSION AR652656.1 GI:67580688
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Preier,S.M.
TITLE Antisense modulation of transforming growth factor-beta 3
expression
JOURNAL Patent: US 6884787-A 75 26-APR-2005;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 58.2%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAAAGCC 22
|||||
Db 18 TACAGGGAGAAAATCC 3

RESULT 8

LOCUS AX405008/c 20 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 25 from Patent WO222634.
ACCESSION AX405008
VERSION AX405008.1 GI:21438223
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Choo,Y. and Isalan,M.
TITLE Method for the preparation of selectively randomised nucleic acid
molecules
JOURNAL Patent: WO 0222634-A 25 21-MAR-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

ORIGIN

Query Match 58.2%; Score 12.8; DB 2; Length 20;
Best Local Similarity 61.1%; Pred. No. 4.8e+05;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGTTACAGGTAGAAAAGC 21
|:::|
Db 19 TSYKCGAGKYAGAAAAGC 2

RESULT 9

LOCUS CQ876341/c 21 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 191 from Patent WO2004065583.
ACCESSION CQ876341
VERSION CQ876341.1 GI:53789945
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cobleigh,M.A., Shak,S., Baker,J.B. and Cronin,M.T.
TITLE Gene expression markers for breast cancer prognosis
JOURNAL Patent: WO 2004065583-A 191 05-AUG-2004;
Genomic Health, Inc. (US); Rush University Medical Center (US)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse primer"

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAAAGCC 22
|
Db 21 TTCTGGTAGAAAAGCC 6

RESULT 10

LOCUS CQ975123/c 21 bp DNA linear PAT 20-JAN-2005
DEFINITION Sequence 80 from Patent WO2004111603.
ACCESSION CQ975123
VERSION CQ975123.1 GI:57999022
KEYWORDS

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SOURCE      synthetic construct
ORGANISM    synthetic constructs; artificial sequences.
REFERENCE   1
AUTHORS     Baker,J.B., Miller,K.D., Shak,S., Sledge,G.W. and Soule,S.U.
TITLE       Gene expression markers for predicting response to chemotherapy
JOURNAL     Patent: WO 2004111603-A 80 23-DEC-2004;
            Genomic Health, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="reverse primer"

ORIGIN
Query Match      58.2%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 TACAGGTAGAAAAGCC 22
Db      21 TTCTGTAGAAAAGCC 6

RESULT 11
CS009834
LOCUS      CS009834
DEFINITION Sequence 66 from Patent WO2005007855.
ACCESSION CS009834
VERSION    CS009834.1 GI:59669672
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic constructs; artificial sequences.
REFERENCE   1
AUTHORS     Usman,N. and Mcswiggen,J.
TITLE       RNA interference mediated inhibition of B7-H1 gene expression using
            short interfering Nucleic Acid (siNA)
JOURNAL     Patent: WO 2005007855-A 66 27-JAN-2005;
            Sirna Therapeutics, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Target
            sequence/siNA sense region"

ORIGIN
Query Match      57.3%; Score 12.6; DB 2; Length 19;
Best Local Similarity 78.9%; Pred. No. 6.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CATGTTACAGGTAGAAAAG 20
Db      1 CCTGTGACAGGAGAAAAG 19

RESULT 12
CS009920/c
LOCUS      CS009920
DEFINITION Sequence 152 from Patent WO2005007855.
ACCESSION CS009920
VERSION    CS009920.1 GI:59669758
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic constructs; artificial sequences.
REFERENCE   1
AUTHORS     Usman,N. and Mcswiggen,J.
TITLE       RNA interference mediated inhibition of B7-H1 gene expression using
            short interfering Nucleic Acid (siNA)

SOURCE      synthetic construct
ORGANISM    synthetic constructs; artificial sequences.
REFERENCE   1
AUTHORS     Baker,J.B., Miller,K.D., Shak,S., Sledge,G.W. and Soule,S.U.
TITLE       Gene expression markers for predicting response to chemotherapy
JOURNAL     Patent: WO 2004111603-A 80 23-DEC-2004;
            Genomic Health, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..19
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            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Target
            sequence/siNA sense region"

ORIGIN
Query Match      57.3%; Score 12.6; DB 2; Length 19;
Best Local Similarity 78.9%; Pred. No. 6.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CATGTTACAGGTAGAAAAG 20
Db      1 CCTGTGACAGGAGAAAAG 19

RESULT 13
CS060643/c
LOCUS      CS060643
DEFINITION Sequence 116 from Patent WO2005028628.
ACCESSION CS060643
VERSION    CS060643.1 GI:62552686
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic constructs; artificial sequences.
REFERENCE   1
AUTHORS     Freier,S.M., Dobie,K.W., Marcusson,E.G., Swayze,E.E., Bhat,B.,
            Graff,J.R. and Konicek,B.W.
TITLE       Modulation of eif4e expression
JOURNAL     Patent: WO 2005028628-A 116 31-MAR-2005;
            Isis Pharmaceuticals, Inc. (US); Eli Lilly and Company (US)
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Antisense Compound"

ORIGIN
Query Match      57.3%; Score 12.6; DB 2; Length 20;
Best Local Similarity 78.9%; Pred. No. 6.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 ATGTTACAGGTAGAAAAGC 21
Db      19 ATGGCTCAAGTAGAAAAGC 1

RESULT 14
CS060728
LOCUS      CS060728
DEFINITION Sequence 201 from Patent WO2005028628.
ACCESSION CS060728
VERSION    CS060728.1 GI:62552771
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Freier,S.M., Dobie,K.W., Marcusson,E.G., Swayze,E.E., Bhat,B.,
            Graff,J.R. and Konicek,B.W.
TITLE       Modulation of eif4e expression
JOURNAL     Patent: WO 2005028628-A 201 31-MAR-2005;
            Isis Pharmaceuticals, Inc. (US); Eli Lilly and Company (US)
FEATURES    Location/Qualifiers
            source
            1..20

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Search completed: June 8, 2006, 22:24:02
Job time : 1978 secs

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OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 21:51:16 ; Search time 2259 Seconds

(without alignments)
544.588 Million cell updates/sec

Title: US-09-743-825-7

Perfect score: 22

Sequence: 1 gcatgtacaggtagaaagcc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 21940

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_est7:*

7: gb_est8:*

8: gb_est9:*

9: gb_est10:*

10: gb_est11:*

11: gb_est12:*

12: gb_est13:*

13: gb_est14:*

14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	13.8	62.7	22	11 AZ659094 1M0536E16
2	11.2	50.9	20	14 T3359P10Q
3	11	50.0	20	11 AL495341 T. brucei
4	10.8	49.1	20	13 AZ452265 1M0252H06
5	10.8	49.1	22	11 CL681335 PRI0130d
6	10.6	48.2	20	11 AZ651001 1M0521O23
7	10.4	47.3	22	11 AZ775974 2M0009H14
8	10.4	47.3	22	11 AZ290555 2M0274N14
9	10.2	46.4	21	14 DU830438 KBX5006K2
10	10	45.5	19	11 AZ649514 1M0519A09
11	10	45.5	19	11 AI545076 fb70d07.y
12	10	45.5	20	11 AZ775273 2M0007F04
13	10	45.5	20	11 AU008116 AU008116
14	10	45.5	21	11 AZ585902 1M0391M24
15	10	45.5	21	11 AZ282823 2M0105B09
16	9.8	44.5	21	11 AZ282823 2M0105B09
17	9.8	44.5	19	5 CF316655 HD--06-A1
18	9.8	44.5	19	11 AZ377971 1M0132I03
19	9.8	44.5	19	11 AZ2808350 2M0071P14
19	9.8	44.5	20	11 AZ625409 1M0464C20

C 20 9.8 44.5 20 11 AZ799032

C 21 9.8 44.5 20 14 AJ596498

C 22 9.8 44.5 21 11 AZ430939

C 23 9.8 44.5 21 11 AZ483078

C 24 9.8 44.5 22 11 AZ786362

C 25 9.6 43.6 19 13 CL668834

C 26 9.6 43.6 20 11 AZ396022

C 27 9.6 43.6 20 11 AZ787298

C 28 9.6 43.6 20 13 CZ443105

C 29 9.6 43.6 20 13 CL687844

C 30 9.6 43.6 21 14 AG197947

C 31 9.6 43.6 22 14 CT013661

C 32 9.4 42.7 19 11 AZ312945

C 33 9.4 42.7 19 11 AZ774536

C 34 9.4 42.7 20 1 AJ796099

C 35 9.4 42.7 21 11 AZ428984

C 36 9.4 42.7 22 11 AZ942905

C 37 9.4 42.7 22 14 TA82F07Q

C 38 9.2 41.8 19 8 CO780477

C 39 9.2 41.8 19 11 AZ612157

C 40 9.2 41.8 19 11 AZ817291

C 41 9.2 41.8 21 1 AU008312

C 42 9.2 41.8 21 11 AZ348213

C 43 9.2 41.8 21 11 AZ760232

C 44 9.2 41.8 21 14 DU835192

C 45 9.2 41.8 22 11 AZ357874

ALIGNMENTS

RESULT 1

AZ659094

LOCUS

DEFINITION

1M0536E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0536E16 F, genomic survey sequence.

ACCESSION

AZ659094

VERSION

AZ659094.1 GI:11796240

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0536 row: E column: 16

Seq primer: CTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

1..22

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0536E16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 62.7%; Score 13.8; DB 11; Length 22;
 Best Local Similarity 88.2%; Pred. No. 7.8e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGTTACAGGTAGAAAA 19
 ||| ||||| ||||| |||||
 Db 6 ATGATACAGGTAGTAA 22

RESULT 2

TA359F10Q/c 20 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA Clone 359f10, reverse sequence,
 genomic survey sequence.

ACCESSION AL495341
 VERSION AL495341.1 GI:11871728
 KEYWORDS GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 20)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrall, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrall, Oxford University Press, 1999).

Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
 1..20
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="359f10"

ORIGIN

Query Match 50.9%; Score 11.2; DB 14; Length 20;
 Best Local Similarity 81.2%; Pred. No. 1.4e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TTACAGGTAGAAAAAGC 21
 ||||| ||||| |||||
 Db 19 TCACAGGCACAAAAGC 4

RESULT 3

AZ452265/c 20 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M025H06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0252H06 F, genomic survey sequence.

ACCESSION AZ452265
 VERSION AZ452265.1 GI:10608897
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0252 row: H column: 06

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0252H06"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."


```

ORIGIN
Query Match      50.0%; Score 11; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACAGGTAGAAA 18
      |||||
      13 ACAGGTAGAAA 3

RESULT 4
CL681335      20 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0130d_E07.2 - PRI0130d.BR (20) Note: Recurring String Mixed
DEFINITION stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL681335.1 GI:50188343
VERSION CL681335
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 20)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
Location/Qualifiers
1..20
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strains="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      49.1%; Score 10.8; DB 13; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.2e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TGTACAGGTAGAA 17
      |||||
      7 TGTGACAGGTAGAA 20

RESULT 5
AZ651001      22 bp DNA linear GSS 14-DEC-2000
LOCUS IM0521023F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0521023 F, genomic survey sequence.
ACCESSION AZ651001
VERSION AZ651001.1 GI:11786054
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0521 row: 0 column: 23
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0521023"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      49.1%; Score 10.8; DB 11; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.2e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TGTACAGGTAGAA 17
      |||||
      6 TGTACAGGTAGAA 19

RESULT 6
AZ775974      20 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0009H14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0009H14 F, genomic survey sequence.
ACCESSION AZ775974.1 GI:12903069
VERSION AZ775974
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS
1 (bases 1 to 20)
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: H column: 14
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0274N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

1. .22
Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0274N14"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 48.2%; Score 10.6; DB 11; Length 20;
Best Local Similarity 76.5%; Pred. No. 2.7e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ATGTACAGGTAGAAA 19
||| ||||| |||||
Db 3 ATGTACAGGTAGAAA 19

RESULT 7

AZ990555/c
LOCUS
DEFINITION
2M0274N14F Mouse 10kb plasmid UUC2M library Mus musculus genomic
clone UUC2M0274N14 F, genomic survey sequence.
ACCESSION
AZ990555
VERSION
AZ990555.1 GI:13861782
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: N column: 14
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

source

1. .22
Location/Qualifiers

ORIGIN

Query Match 47.3%; Score 10.4; DB 11; Length 22;
Best Local Similarity 91.7%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAA 18
||||| |||||
Db 13 TGCAGGTAGAAA 2

RESULT 8

DUB30438
LOCUS
DEFINITION
DUB30438 22 bp DNA linear GSS 22-DEC-2005
KBR-S006K24F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBR-S006K24, genomic survey
sequence.
DUB30438
ACCESSION
DUB30438
VERSION
DUB30438.1 GI:83867034
KEYWORDS
GSS.

SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
TITLE
JOURNAL
COMMENT
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS006K24
Seq primer: T7
Class: BAC ends.
FEATURES
source
1. .22
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
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/clone="KBrS006K24"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIB."

ORIGIN
Query Match 47.3%; Score 10.4; DB 14; Length 22;
Best Local Similarity 91.7%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 GGTAGAAAAGCC 22
|||||
DB 4 GGTAGAAAACC 15
|||||

RESULT 9
AZ649514/c
LOCUS
DEFINITION
1M0519A09P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0519A09 F, genomic survey sequence.
ACCESSION
AZ649514
VERSION
AZ649514.1 GI:11783070
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
TITLE
JOURNAL
COMMENT
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS006K24
Seq primer: T7
Class: BAC ends.
FEATURES
source
1. .22
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS006K24"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIB."

ORIGIN
Query Match 47.3%; Score 10.4; DB 14; Length 22;
Best Local Similarity 91.7%; Pred. No. 3.4e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 GGTAGAAAAGCC 22
|||||
DB 4 GGTAGAAAACC 15
|||||

RESULT 9
AZ649514/c
LOCUS
DEFINITION
1M0519A09P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0519A09 F, genomic survey sequence.
ACCESSION
AZ649514
VERSION
AZ649514.1 GI:11783070
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0519 row: A column: 09
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0519A09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 46.4%; Score 10.2; DB 11; Length 21;
Best Local Similarity 80.0%; Pred. No. 4.3e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 TTACAGGTAGAAAAG 20
|||||
DB 16 TTGACGGTATTAAAG 2
|||||

RESULT 10
AI545076
LOCUS
DEFINITION
AI545076 19 bp mRNA linear EST 07-JUN-2001
fb70d07.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3717229 5', similar to TR:023327 023327 HYPOTHETICAL 108.0 KD
PROTEIN. ;, mRNA sequence.
ACCESSION
AI545076
VERSION
AI545076.1 GI:4462449
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
AUTHORS
1 (bases 1 to 19)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
TITLE
JOURNAL
COMMENT
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimatDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: T3 ET from Amersham

High quality sequence stop: 1

POLYA=No.

FEATURES

source

1..19
Location/Qualifiers

/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3717229"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLA-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
strand cDNA was primed with a NotI oligo(dT)15 primer
(5'-GCACGAGTCTAGATCGAGCGCCCTTTTCTTTTCTTTT3');
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

ORIGIN

Query Match 45.5%; Score 10; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. NO. 5.2e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGTAGAAA 18
|||||
Db 2 GCATGGTACATGGATGAA 19

RESULT 11

AZ775273/c
LOCUS AZ775273 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0007F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0007F04 R, genomic survey sequence.

ACCESSION AZ775273

VERSION AZ775273.1 GI:12901587

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE

JOURNAL

COMMENT

Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0007 row: F column: 04

Seq primer: CACACAGGAAACAGCATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0007F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 45.5%; Score 10; DB 11; Length 19;
Best Local Similarity 72.2%; Pred. No. 5.2e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TGTTCAGGTAGAAAAGC 21
|||||
Db 18 TGCCACAGGAAAAACGC 1

RESULT 12

AU008116/c

LOCUS AU008116 20 bp mRNA linear EST 31-JUL-1998

DEFINITION AU008116 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc02889, mRNA sequence.

ACCESSION AU008116

VERSION AU008116.1 GI:3344574

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM

Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.

1 (bases 1 to 20)

Morimyo, M. and Mita, K.

REFERENCE

1 Identification of expressed sequence tags of Schizosaccharomyces

JOURNAL
 COMMENT
 Unpublished (1998)
 Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp

FEATURES
 source
 1..20
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="gpc02889"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN
 Query Match 45.5%; Score 10; DB 1; Length 20;
 Best Local Similarity 72.2%; Pred. No. 5.3e+06;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCATGTTACAGGTAGAA 18
 |||||
 Db 20 GCGTGTAAAGGAATACA 3

RESULT 13
 AZ585902
 LOCUS
 DEFINITION
 1M0391M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391M24 F, genomic survey sequence.

ACCESSION
 AZ585902
 VERSION
 AZ585902.1 GI:11708092
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus
 Mus musculus (house mouse)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0391 row: M column: 24
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

pombe
 Unpublished (1998)
 Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp

FEATURES
 source
 1..20
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="gpc02889"
 /sex="h minus"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN
 Query Match 45.5%; Score 10; DB 1; Length 20;
 Best Local Similarity 72.2%; Pred. No. 5.3e+06;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCATGTTACAGGTAGAA 18
 |||||
 Db 20 GCGTGTAAAGGAATACA 3

RESULT 14
 AZ828233
 LOCUS
 DEFINITION
 2M0105B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0105B09 F, genomic survey sequence.

ACCESSION
 AZ828233
 VERSION
 AZ828233.1 GI:12998141
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus
 Mus musculus (house mouse)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0105 row: B column: 09
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"

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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 45.5%; Score 10; DB 11; Length 20;
 Best Local Similarity 72.2%; Pred. No. 5.3e+06;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGTTCACAGGTAGAAAGC 21
 |||||
 Db 1 TGATACAGGAGTAAAC 18

RESULT 14
 AZ828233
 LOCUS
 DEFINITION
 2M0105B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0105B09 F, genomic survey sequence.

ACCESSION
 AZ828233
 VERSION
 AZ828233.1 GI:12998141
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus
 Mus musculus (house mouse)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0105 row: B column: 09
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone="UUGC2M0105B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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ORIGIN

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Query Match      45.5%; Score 10; DB 11; Length 21;
Best Local Similarity 72.2%; Pred. No. 5.3e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2 CATGTTACAGGTAGAAA 19
    ||||| ||| ||| |||
DB   2 CCTGTAAACAATTAAAAA 19

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RESULT 15

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AZ828233/c
LOCUS      2M0105B09F Mouse 10kb plasmid UUGC1M library Mus musculus Genomic
DEFINITION clone UUGC2M0105B09 F, genomic survey sequence.
ACCESSION  AZ828233
VERSION    AZ828233.1 GI:12998141
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

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TITLE

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

```

COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: B column: 09
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"

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FEATURES

source

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

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Query Match      45.5%; Score 10; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 TGTTCACAGGT 13
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DB   10 TGTTCACAGGT 1

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Search completed: June 8, 2006, 23:01:53

Job time : 2264 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 22:10:54 ; Search time 100 Seconds
(without alignments)
411.644 Million cell updates/sec

Title: US-09-743-825-7

Perfect score: 22

Sequence: 1 gcatgtacagtagaagacc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 576012

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
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- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	13.2	60.0	21	3	US-09-689-065B-50
3	13.2	60.0	21	4	US-10-210-296A-50
C 4	12.8	58.2	19	3	US-09-564-805-157
C 5	12.8	58.2	19	3	US-09-434-382-157
C 6	12.8	58.2	20	3	US-09-906-158-75
7	12.2	55.5	18	3	US-08-840-316-53
8	12.2	55.5	18	3	US-08-809-523-53
9	12.2	55.5	18	3	US-08-471-971-53
10	12.2	55.5	18	3	US-09-402-776-53
11	12.2	55.5	18	3	US-09-422-978-4779
12	12.2	55.5	18	3	US-08-470-246-53
13	12.2	55.5	18	3	US-08-316-765-53
14	12.2	55.5	18	3	US-09-724-475-53
15	12.2	55.5	18	7	PCT-US93-08849A-53
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C 17	12.2	55.5	20	3	US-09-702-251-44
18	12.2	55.5	20	3	US-08-765-340-23
C 19	12.2	55.5	20	3	US-09-422-978-9693
C 20	12.2	55.5	21	3	US-09-696-791-4514
21	11.8	53.6	19	3	US-09-422-978-6072
C 22	11.8	53.6	20	2	US-08-477-270-27
23	11.8	53.6	20	3	US-09-487-445-98

C	24	11.6	52.7	19	3	US-09-648-520B-29	Sequence 29, Appl
	25	11.6	52.7	19	3	US-09-422-978-4544	Sequence 4544, Ap
	26	11.4	51.8	17	3	US-08-985-162-702	Sequence 702, App
	27	11.4	51.8	17	3	US-08-985-162-703	Sequence 703, App
	28	11.4	51.8	17	3	US-08-985-162-704	Sequence 704, App
	29	11.4	51.8	17	3	US-08-985-162-705	Sequence 705, App
	30	11.4	51.8	17	3	US-08-584-040-1534	Sequence 1534, Ap
	31	11.4	51.8	17	3	US-09-371-772B-79	Sequence 79, Appl
	32	11.4	51.8	17	3	US-09-371-772B-4284	Sequence 4284, Ap
	33	11.4	51.8	17	3	US-09-401-063-702	Sequence 702, App
	34	11.4	51.8	17	3	US-09-401-063-703	Sequence 703, App
	35	11.4	51.8	17	3	US-09-401-063-704	Sequence 704, App
	36	11.4	51.8	17	3	US-09-401-063-705	Sequence 705, App
	37	11.4	51.8	17	3	US-09-685-664B-79	Sequence 79, Appl
	38	11.4	51.8	17	5	US-10-138-674B-79	Sequence 79, Appl
	39	11.4	51.8	17	5	US-10-138-674B-4284	Sequence 4284, Ap
	40	11.4	51.8	17	5	US-10-138-674B-7261	Sequence 7261, Ap
	41	11.4	51.8	18	3	US-08-981-988A-27	Sequence 27, Appl
	42	11.4	51.8	19	3	US-09-531-000-7	Sequence 7, Appl
	43	11.4	51.8	19	3	US-09-531-000-34	Sequence 34, Appl
	44	11.4	51.8	19	3	US-09-531-000-38	Sequence 38, Appl
	45	11.4	51.8	19	3	US-09-422-978-6684	Sequence 6684, Ap

ALIGNMENTS

RESULT 1

US-09-198-452A-5333/c
; Sequence 5333, Application US/09198452A
; Patent No. 6559294

GENERAL INFORMATION:

; APPLICANT: Griffiths, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 5333

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-5333

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Best Local Similarity 85.0%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGTTACAGGTAGAAAAG 20
Db 20 GCCTGTTCCAGATAGAAAAG 1

RESULT 2

US-09-689-065B-50

; Sequence 50, Application US/09689065B

; Patent No. 6605596

GENERAL INFORMATION:

; APPLICANT: Pfizer Products, Inc.

; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND

; FILE REFERENCE: 3153.00187/PC10589A

; CURRENT APPLICATION NUMBER: US/09/689,065B

; CURRENT FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: US Prov. 60/160,922

; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: US Prov. 60/163,858

; PRIOR FILING DATE: 1999-11-05

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 50

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; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-09-689-065B-50

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Best Local Similarity 83.3%; Pred. No. 4.6e+03;
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   ||||| ||||| |||||
Db 2 TGGTACACGACAGAAAAGC 19

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; Sequence 50, Application US/10210296A
; Patent No. 6982314
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products, Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED METHODS AND
; FILE REFERENCE: 3153.00355/PC10589B
; CURRENT APPLICATION NUMBER: US/10/210,296A
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/689,065
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/160,922
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/163,858
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-10-210-296A-50

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Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGTTCACAGGTAGAAAAGC 21
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Db 2 TGGTACACGACAGAAAAGC 19

RESULT 4
US-09-564-805-157/c
; Sequence 157, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: Gene and a Paralog and Orthologous Genes
; CURRENT APPLICATION NUMBER: US/09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-564-805-157

Query Match      58.2%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 7.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGTTACAGGTAGAAA 18
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Db 19 ATGTCACAGGCAGAAA 4

RESULT 5
US-09-434-382-157/c
; Sequence 157, Application US/09434382
; Patent No. 6844189
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: HPC2 Gene
; CURRENT APPLICATION NUMBER: US/09/434,382
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: US 60/107,468
; EARLIER FILING DATE: 1999-11-06
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-434-382-157

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Best Local Similarity 87.5%; Pred. No. 7.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGTTACAGGTAGAAA 18
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Db 19 ATGTCACAGGCAGAAA 4

RESULT 6
US-09-906-158-75/c
; Sequence 75, Application US/09906158
; Patent No. 6884787
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESS
; FILE REFERENCE: RTS-0257
; CURRENT APPLICATION NUMBER: US/09/906,158
; CURRENT FILING DATE: 2001-07-14
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-906-158-75

Query Match      58.2%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 7.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TACAGGTAGAAAAGCC 22
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Db 18 TACAGGGAGAAAATCC 3

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RESULT 7
US-08-840-316-53
; Sequence 53, Application US/08840316
; Patent No. 6054567
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tearev, Sergei. A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,316
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-840-316-53

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Query Match 55.5%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GTTACAGGTAGAAAAGC 21
Db 2 GTTACAGCCAGAAAACC 18

RESULT 8
US-08-809-523-53
; Sequence 53, Application US/08809523
; Patent No. 6207416
; GENERAL INFORMATION:
; APPLICANT: Emerson, Sergei. A., Emerson,
; APPLICANT: Tearev, Sergei. A., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA

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; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,523
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13102
; FILING DATE: 03-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-809-523-53

Query Match 55.5%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GTTACAGGTAGAAAAGC 21
Db 2 GTTACAGCCAGAAAACC 18

RESULT 9
US-08-471-971-53
; Sequence 53, Application US/08471971
; Patent No. 6287759
; GENERAL INFORMATION:
; APPLICANT: Tearev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,971
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; CLASSIFICATION: 435

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US07/947,263
;; FILING DATE: 18-SEP-1992
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard W. Bork
;; REGISTRATION NUMBER: 36,459
;; REFERENCE/DOCKET NUMBER: 2026-4032US2
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-471-971-53

Query Match 55.5%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GTTACAGGTAGAAAAC 21
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Db 2 GTTACAGCCAGAAAAC 18

RESULT 10
US-09-402-776-53
; Sequence 53, Application US/09402776
; Patent No. 6458562
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tsarev, Sergei A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/402,776
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/840,316
;; FILING DATE: 11-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard W. Bork
;; REGISTRATION NUMBER: 36,459
;; REFERENCE/DOCKET NUMBER: 2026-4255
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

US-09-402-776-53

Query Match 55.5%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 GTTACAGGTAGAAAAC 21
| | | | | | | | | | | | | | | | | |
Db 2 GTTACAGCCAGAAAAC 18

RESULT 11
US-09-422-978-4779
; Sequence 4779, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4779
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-09-422-978-4779

Query Match 55.5%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTCAGGTAGAAAAG 20
| | | | | | | | | | | | | | | | | |
Db 1 TGTGAGAGGTAGAGAAG 17

RESULT 12
US-08-470-246-53
; Sequence 53, Application US/08470246
; Patent No. 6696242
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,246
; FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-246-53
Query Match
Best Local Similarity 55.5%; Score 12.2; DB 3; Length 18;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 GTTACAGGTAGAAAAGC 21
Db 2 GTTACAGCCAGAAAACC 18
RESULT 13
US-08-765-53
Sequence 53, Application US/08316765
Patent No. 6706873
GENERAL INFORMATION:
APPLICANT: Tsarev, Sergei. A.; Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-316-765-53
Query Match
Best Local Similarity 55.5%; Score 12.2; DB 3; Length 18;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 GTTACAGGTAGAAAAGC 21
Db 2 GTTACAGCCAGAAAACC 18
RESULT 14
US-09-724-475-53
Sequence 53, Application US/09724475
Patent No. 6787145
GENERAL INFORMATION:
APPLICANT: Tsarev, Sergei. A.; Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,475
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,523
FILING DATE: <Unknown>
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-724-475-53
Query Match
Best Local Similarity 55.5%; Score 12.2; DB 3; Length 18;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 GTTACAGGTAGAAAAGC 21
Db 2 GTTACAGCCAGAAAACC 18

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RESULT 15
PCT-US93-08849A-53
; Sequence 53, Application PC/TUS9308849A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849A
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William S. Feller
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4032 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-08849A-53

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Query Match      55.5%; Score 12.2; DB 7; Length 18;
Best Local Similarity 82.4%; Pred. NO. 1.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 GTTACAGGTAGAAAGC 21
Db      2 GTTACAGCCAGAAACC 18

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Search completed: June 8, 2006, 22:48:58
Job time : 101 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 22:49:19 ; Search time 857 Seconds
(without alignments)
315.435 Million cell updates/sec

Title: US-09-743-825-7

Perfect score: 22

Sequence: 1 gcattgtacagtagaagc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 10729360

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.2	69.1	20	7	US-10-289-762-5333 Sequence 5333, Ap
2	14.6	66.4	22	11	US-10-310-914A-1053240 Sequence 1053240, Ap
3	14.4	65.5	20	11	US-10-310-914A-163654 Sequence 163654, Ap
4	14.2	64.5	22	11	US-10-310-914A-344929 Sequence 344929, Ap
C 5	13.8	62.7	19	14	US-11-083-784-920023 Sequence 920023, Ap
6	13.8	62.7	19	14	US-11-083-784-935948 Sequence 935948, Ap
C 7	13.8	62.7	19	15	US-11-101-244-920023 Sequence 920023, Ap
8	13.8	62.7	19	15	US-11-101-244-935948 Sequence 935948, Ap
9	13.8	62.7	21	11	US-10-310-914A-353174 Sequence 353174, Ap
C 10	13.8	62.7	21	11	US-10-310-914A-805859 Sequence 805859, Ap
11	13.8	62.7	22	11	US-10-310-914A-353175 Sequence 353175, Ap
12	13.4	60.9	22	11	US-10-310-914A-117024 Sequence 117024, Ap
13	13.4	60.9	22	11	US-10-310-914A-464518 Sequence 464518, Ap
C 14	13.4	60.9	22	11	US-10-310-914A-574946 Sequence 574946, Ap
C 15	13.2	60.0	19	11	US-10-310-914A-361013 Sequence 361013, Ap
16	13.2	60.0	19	14	US-11-083-784-29724, A
17	13.2	60.0	19	14	US-11-083-784-1359984, A

ALIGNMENTS

RESULT 1

US-10-289-762-5333/c

; Sequence 5333, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Grifflair, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 5333

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-5333

Query Match 69.1%; Score 15.2; DB 7; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGGTAGAAAAG 20

Db 20 GCCTGTTCCAGATAGAAAAG 1

RESULT 2

US-10-310-914A-1053240

; Sequence 1053240, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiller, Kruzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CFUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

Sequence 29724, A
Sequence 1359984,
Sequence 225688,
Sequence 50, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 248351,
Sequence 566298,
Sequence 221112,
Sequence 157, App
Sequence 157, App
Sequence 395658,
Sequence 486688,
Sequence 651437,
Sequence 147360,
Sequence 614693,
Sequence 676530,
Sequence 683977,
Sequence 948986,
Sequence 949038,
Sequence 1321930,
Sequence 1517314,
Sequence 1519873,
Sequence 1519908,
Sequence 147360,
Sequence 614693,
Sequence 676530,

18 13.2 60.0 19 15 US-11-101-244-29724
19 13.2 60.0 19 15 US-11-101-244-1359984
20 13.2 60.0 20 11 US-10-310-914A-225688
21 13.2 60.0 21 6 US-10-210-296-50
22 13.2 60.0 21 7 US-10-449-462-50
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24 13.2 60.0 22 11 US-10-310-914A-248351
25 13.2 60.0 22 11 US-10-310-914A-566298
26 12.8 58.2 18 11 US-10-310-914A-221112
27 12.8 58.2 19 3 US-09-988-626-157
28 12.8 58.2 19 3 US-09-988-687-157
29 12.8 58.2 19 3 US-09-988-686-157
30 12.8 58.2 19 11 US-10-310-914A-395658
31 12.8 58.2 19 11 US-10-310-914A-486688
32 12.8 58.2 19 11 US-10-310-914A-651437
33 12.8 58.2 19 14 US-11-083-784-147360
34 12.8 58.2 19 14 US-11-083-784-614693
35 12.8 58.2 19 14 US-11-083-784-676530
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39 12.8 58.2 19 14 US-11-083-784-1321930
40 12.8 58.2 19 14 US-11-083-784-1517314
41 12.8 58.2 19 14 US-11-083-784-1519873
42 12.8 58.2 19 14 US-11-083-784-1519908
43 12.8 58.2 19 15 US-11-101-244-147360
44 12.8 58.2 19 15 US-11-101-244-614693
45 12.8 58.2 19 15 US-11-101-244-676530

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; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1053240
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053240

Query Match      66.4%; Score 14.6; DB 11; Length 22;
Best Local Similarity 61.9%; Pred. No. 6.5e+03;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy  2 CATGTTACAGGTAGAAAAGCC 22
    ||: :: ||||: |||| ||
Db  2 CAUUUCCAGGUGGAAAAAAC 22

RESULT 3
US-10-310-914A-163654
; Sequence 163654, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 163654
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-163654

Query Match      65.5%; Score 14.4; DB 11; Length 20;
Best Local Similarity 81.2%; Pred. No. 8e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  7 TACAGGTAGAAAAGCC 22
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Db  3 UACAGGUAGUAAGCC 18

RESULT 4
US-10-310-914A-344929
; Sequence 344929, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 344929
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-344929

Query Match      64.5%; Score 14.2; DB 11; Length 22;
Best Local Similarity 73.7%; Pred. No. 1e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  3 ATGTTACAGGTAGAAAAGCC 21
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Db  2 AUGUGACAGGCGAUAAGC 20
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RESULT 5
US-11-083-784-920023/c
; Sequence 920023, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 920023
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-920023

Query Match      62.7%; Score 13.8; DB 14; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 ATGTTACAGGTAGAAAA 19
    ||||| ||||| |||
Db  17 AGGTTACAGGTAGGAAA 1

RESULT 6
US-11-083-784-935948
; Sequence 935948, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 935948
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-935948

Query Match      62.7%; Score 13.8; DB 14; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.6e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 2 CATGTTACAGGTAGAAA 18
|||::|||::|||::|||
Db 1 CAAGUUAUACAUAGAGAA 17

RESULT 7
US-11-101-244-920023/c
; Sequence 920023, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 920023
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-920023

Query Match 62.7%; Score 13.8; DB 15; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGTTACAGGTAGAAA 19
|||::|||::|||::|||
Db 17 AGGTTACAGGTAGAAA 1

RESULT 8
US-11-101-244-935948
; Sequence 935948, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 935948
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-935948

Query Match 62.7%; Score 13.8; DB 15; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.6e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATGTTACAGGTAGAAA 18

Db 1 CAAGUUAUACAUAGAGAA 17
|||::|||::|||::|||

RESULT 9
US-10-310-914A-353174
; Sequence 353174, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 353174
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-353174

Query Match 62.7%; Score 13.8; DB 11; Length 21;
Best Local Similarity 70.6%; Pred. No. 1.6e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGTTCACAGGTAGAAAAG 20
|||::|||::|||::|||
Db 3 UGUUACAGGAAGAGAG 19

RESULT 10
US-10-310-914A-805859/c
; Sequence 805859, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 805859
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-805859

Query Match 62.7%; Score 13.8; DB 11; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGTTACAGGTAGAA 17
|||::|||::|||::|||
Db 21 GCATGTTACAGGTAGAA 5

RESULT 11
US-10-310-914A-353175
; Sequence 353175, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 353175
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-353175

Query Match 62.7%; Score 13.8; DB 11; Length 22;
Best Local Similarity 70.6%; Pred. No. 1.6e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGTACAGGTAGAAAAG 20
:|||||
Db 3 UGUUACAGGAAGAAG 19

RESULT 12
US-10-310-914A-117024
; Sequence 117024, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117024
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-117024

Query Match 60.9%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 2.5e+04;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACAGGTAGAAAAGCC 22
|||||
Db 5 ACAGCUAGAAAAGCC 19

RESULT 13
US-10-310-914A-464518
; Sequence 464518, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 464518
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-464518

Query Match 60.9%; Score 13.4; DB 11; Length 22;
Best Local Similarity 93.3%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ACAGGTAGAAAAGCC 22
|||||

Db 7 ACAGGAGAAAAGCC 21

RESULT 14

US-10-310-914A-574946/c
; Sequence 574946, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 574946
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-574946

Query Match 60.9%; Score 13.4; DB 11; Length 22;
Best Local Similarity 93.3%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGTACAGGTAGAAA 18
|||||
Db 15 TGTTCAGGTAGAAA 1

RESULT 15

US-10-310-914A-361013/c
; Sequence 361013, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 361013
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-361013

Query Match 60.0%; Score 13.2; DB 11; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GTTACAGGTAGAAAAGCC 22
|||||
Db 19 GTTACATGTAGAAAAGCCC 2

Search completed: June 8, 2006, 23:04:06
Job time : 858 secs

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications_databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New_databases: older published applications make up the Published_Applications_Main_databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 22:49:54 ; Search time 23 Seconds
(without alignments)
121.405 Million cell updates/sec

Title: US-09-743-825-7

Perfect score: 22

Sequence: 1 gcagttagaggtagaagcc 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 22518

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB_seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB_seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB_seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB_seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB_seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB_seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB_seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ref ID	No.	Score	Query Match	Length	DB ID	Description
C	1	12.8	58.2	21	7	US-11-242-111-36
C	2	11	50.0	22	7	US-11-222-810-30
C	3	10.8	49.1	18	7	US-11-293-697-5192
C	4	10.8	49.1	21	6	US-10-511-937-1101
	5	10.6	48.2	20	7	US-11-189-279-44
	6	10.4	47.3	18	7	US-11-293-697-5279
C	7	10	45.5	22	7	US-11-264-558-29
	8	9.8	44.5	18	7	US-11-293-697-5086
C	9	9.8	44.5	20	7	US-11-189-597-5
C	10	9.8	44.5	20	7	US-11-255-980-60
C	11	9.8	44.5	21	6	US-10-559-415-155
	12	9.6	43.6	19	7	US-11-251-465-425
	13	9.6	43.6	21	7	US-11-251-465-426
	14	9.6	43.6	22	6	US-10-148-883-38
	15	9.4	42.7	18	7	US-11-293-697-5297
	16	9.4	42.7	19	7	US-11-200-624-12
	17	9.4	42.7	20	6	US-10-511-937-1889
	18	9.4	42.7	20	6	US-10-469-938A-23
C	19	9.4	42.7	21	7	US-11-254-173-11
C	20	9.4	42.7	21	7	US-11-264-784-302
C	21	9.4	42.7	21	7	US-11-264-737-412
C	22	9.4	42.7	21	7	US-11-265-761-314
	23	9.4	42.7	22	7	US-11-524-524-39
	24	9.2	41.8	19	7	US-11-200-624-35
	25	9.2	41.8	20	6	US-10-511-455-77

26	9.2	41.8	20	6	US-10-511-832-90	Sequence 90, Appl
C 27	9.2	41.8	21	6	US-10-511-937-1865	Sequence 1865, App
C 28	9.2	41.8	21	7	US-11-078-073-406	Sequence 406, App
29	9.2	41.8	21	7	US-11-078-073-407	Sequence 407, App
30	9.2	41.8	22	6	US-10-511-937-868	Sequence 868, App
31	9.2	41.8	22	6	US-10-514-776-62	Sequence 62, Appl
C 32	9	40.9	11	7	US-11-158-209-920	Sequence 920, App
C 33	9	40.9	18	7	US-11-252-276-107	Sequence 107, App
C 34	9	40.9	18	7	US-11-252-276-111	Sequence 111, App
35	9	40.9	20	6	US-10-559-415-143	Sequence 143, App
36	9	40.9	21	1	US-09-756-097B-98	Sequence 98, Appl
C 37	9	40.9	21	6	US-10-469-938A-41	Sequence 41, Appl
C 38	9	40.9	22	6	US-10-469-938A-122	Sequence 122, App
C 39	9	40.9	22	6	US-10-553-238-59	Sequence 59, Appl
40	9	40.9	22	7	US-11-242-139-168	Sequence 168, App
41	9	40.9	22	7	US-11-265-052-19	Sequence 19, Appl
42	9	40.9	22	7	US-11-265-065-19	Sequence 19, Appl
C 43	9	40.9	22	7	US-11-321-421-181	Sequence 181, App
C 44	8.8	40.0	18	6	US-10-520-094-13	Sequence 13, Appl
C 45	8.8	40.0	18	7	US-11-293-697-5420	Sequence 5420, App

ALIGNMENTS

RESULT 1

US-11-242-111-36/c
; Sequence 36, Application US/11242111
; Publication No. US2006008862A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M
; TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION
; FILE REFERENCE: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEROF
; CURRENT APPLICATION NUMBER: US/11/242.111
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 60/614,746
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/651,344
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
US-11-242-111-36

Query Match 58.2%; Score 12.8; DB 7; Length 21;
Best Local Similarity 87.5%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAAAGCC 22
Db 21 TTCTGTTAGAAAAGCC 6

RESULT 2

US-11-222-810-30/c
; Sequence 30, Application US/11222810
; Publication No. US20060089490A1
; GENERAL INFORMATION:
; APPLICANT: MELKI, Judith
; APPLICANT: MUNNICH, Arnold
; TITLE OF INVENTION: Spinal Muscular Atrophy Diagnostic Methods
; FILE REFERENCE: 2121-0140P
; CURRENT APPLICATION NUMBER: US/11/222,810
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/109,082
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 08/545,196
; PRIOR FILING DATE: 1995-10-19
; NUMBER OF SEQ ID NOS: 65

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; SOFTWARE: PatentIn version 3.2

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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CAGGTAGAAAAG 20
||| |||||
Db 5 CAGATAGAAAAG 16

RESULT 7

US-11-264-558-29/c
; Sequence 29, Application US/11264558
; Publication No. US20060088913A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; APPLICANT: Harkin, Louise A
; APPLICANT: Dibbens, Leanne M
; TITLE OF INVENTION: MUTATION ASSOCIATED WITH EPILEPSY
; FILE REFERENCE: 1386/10/2
; CURRENT APPLICATION NUMBER: US/11/264,558
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: US 10/312,184
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/AU01/00729
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-264-558-29

Query Match 45.5%; Score 10; DB 7; Length 22;
Best Local Similarity 72.2%; Pred. No. 9.9e+03;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GTTACAGGTAGAAAGCC 22
| || ||||| |||
Db 22 GGTAGAGGTAGGAGACCC 5

RESULT 8

US-11-293-697-5086
; Sequence 5086, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5086
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p

Query Match 44.5%; Score 9.8; DB 7; Length 18;
Best Local Similarity 84.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CAGGTAGAAAAGC 21
||| |||||
Db 4 CAGGTAGAAAACC 16

RESULT 9

US-11-189-597-5/c
; Sequence 5, Application US/11189597
; Publication No. US20060089299A1
; GENERAL INFORMATION:
; APPLICANT: HSIANG, York
; APPLICANT: BUCHAN, Alison
; APPLICANT: LEVY, Julia G.
; APPLICANT: MARGARON, Philippe Maria Clotaire
; TITLE OF INVENTION: SELECTIVE TREATMENT OF ENDOTHELIAL SOMATOSTATIN RECEPTORS
; FILE REFERENCE: 249692001101
; CURRENT APPLICATION NUMBER: US/11/189,597
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: US 09/797,779
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/CA99/008800
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: CA 2,246,791
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human SSTR3 primer
US-11-189-597-5

Query Match 44.5%; Score 9.8; DB 7; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCATGTTACAGGT 13
||| |||||
Db 17 GCATGTGCACGT 5

RESULT 10

US-11-255-980-60/c
; Sequence 60, Application US/11255980
; Publication No. US20060115844A1
; GENERAL INFORMATION:
; APPLICANT: FINKELSTEIN, SYDNEY DAVID
; APPLICANT: SWALSKY, PATRICIA
; TITLE OF INVENTION: ENHANCED AMPLIFIABILITY OF MINUTE FIXATIVE-TREATED
; TITLE OF INVENTION: TISSUE SAMPLES, MINUTE STAINED CYTOLOGY SAMPLES, AND
; TITLE OF INVENTION: OTHER MINUTE SOURCES OF DNA
; FILE REFERENCE: 47030.0014-01US
; CURRENT APPLICATION NUMBER: US/11/255,980
; CURRENT FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: 60/679,969
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/679,968
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/644,568
; PRIOR FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: 60/631,240
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/620,926
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-255-980-60

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Query Match          44.5%; Score 9.8; DB 7; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGT 13
Db 19 GCATATTACTGGT 7

RESULT 11
US-10-559-415-155/c
; Sequence 155, Application US/10559415
; Publication No. US20060100132A1
; GENERAL INFORMATION:
; APPLICANT: AstraZeneca AB et al
; TITLE OF INVENTION: Diagnostic Method
; FILE REFERENCE: 101073-1P WO
; CURRENT APPLICATION NUMBER: US/10/559,415
; CURRENT FILING DATE: 2003-12-06
; PRIOR APPLICATION NUMBER: 0313081.2
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 155
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-559-415-155

Query Match          44.5%; Score 9.8; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 AGGTAGAAAGCC 22
Db 19 AGGCAGTAAGCC 7

RESULT 12
US-11-251-465-425
; Sequence 425, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 425
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-425

Query Match          43.6%; Score 9.6; DB 7; Length 22;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CATGTTACAGTAGAA 17
Db 2 CATGTCGAGTAGAA 17

RESULT 13
US-11-251-465-426
; Sequence 426, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-426

Query Match          43.6%; Score 9.6; DB 6; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CATGTTACAGTAGAA 17
Db 4 CATGTCGAGTAGAA 19

RESULT 14
US-10-148-883-38
; Sequence 38, Application US/10148883
; Publication No. US20060115811A1
; GENERAL INFORMATION:
; APPLICANT: Jay White et al.
; TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins
; FILE REFERENCE: 11812-49
; CURRENT APPLICATION NUMBER: US/10/148,883
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 60/171,110
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 60/178,314
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-148-883-38

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Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAAGCC 22
Db 3 TCCAGGTAGCGCAGCC 18

RESULT 15
US-11-293-697-5297
; Sequence 5297, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
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; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5297
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-11-293-697-5297

Query Match      42.7%; Score 9.4; DB 7; Length 18;
Best Local Similarity 90.9%; Pred. No. 1.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      7 ACAGGAAGAAA 17

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Perfect score: 21

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Scoring table: IDENTITY_NUC

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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1150878

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	61.9	20	2	AR116690 Sequence
2	13	61.9	20	2	AR275648 Sequence
3	12.8	61.0	17	2	BD067608 Enzymatic
4	12.8	61.0	17	2	AR402108 Sequence
5	12.8	61.0	20	2	AL7234 Oligonucleo
6	12.8	61.0	20	2	AR027617 Sequence
7	12.8	61.0	21	2	DD206720 RNA Inter
8	12.8	61.0	21	2	DD206724 RNA Inter
9	12.8	61.0	21	2	DD206728 RNA Inter
10	12.8	61.0	21	2	DD206732 RNA Inter
11	12.8	61.0	21	2	DD206736 RNA Inter
12	12.8	61.0	21	2	DD206740 RNA Inter
13	12.8	61.0	21	2	DD207467 RNA Inter
14	12.8	61.0	21	2	DD207470 RNA Inter
15	12.8	61.0	21	2	DD207473 RNA Inter
16	12.8	61.0	21	2	DD207477 RNA Inter
17	12.2	58.1	17	2	BD067609 Enzymatic
18	12.2	58.1	17	2	AR402109 Sequence

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	20	12.2	58.1	20	2	AR070817	AR070817	Sequence
	21	12.2	58.1	20	2	AR104505	AR104505	Sequence
c	22	12.2	58.1	20	2	AX962823	AX962823	Sequence
c	23	12	57.1	17	2	AX737882	AX737882	Sequence
	24	12	57.1	21	2	CS018067	CS018067	Sequence
	25	12	57.1	21	2	CS037179	CS037179	Sequence
	26	11.8	56.2	16	2	AR328335	AR328335	Sequence
	27	11.8	56.2	17	2	AR007304	AR007304	Sequence
	28	11.8	56.2	17	2	AR053990	AR053990	Sequence
c	29	11.8	56.2	17	2	AR135992	AR135992	Sequence
	30	11.8	56.2	17	2	BD067607	BD067607	Enzymatic
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	32	11.8	56.2	17	2	AR327036	AR327036	Sequence
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c	34	11.8	56.2	17	2	AX217836	AX217836	Sequence
c	35	11.8	56.2	20	2	AR160744	AR160744	Sequence
c	36	11.8	56.2	20	2	AR310829	AR310829	Sequence
c	37	11.8	56.2	21	2	BD238283	BD238283	Accelerat
c	38	11.8	56.2	21	2	DD176955	DD176955	Verificat
c	39	11.8	56.2	21	2	AX804694	AX804694	Sequence
c	40	11.8	56.2	21	7	DGCG00505A	L77539 Canis fami1	
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c	45	11.6	55.2	20	2	BD128305	BD128305	Utilizati

ALIGNMENTS

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DEFINITION AR116690
ACCESSION AR116690
VERSION AR116690.1 GI:14097012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buell,G.Nutter., Surprenant,A. and Kawashima,E.
TITLE Purinergic receptor
JOURNAL Patent: US 6133434-A 3 17-OCT-2000;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCCTATCTGAAG 15
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Db 1 GGCCTATCTGAAG 13
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LOCUS AR275648 Sequence 3 from patent US 6509163. linear DNA 20 bp PAT 10-APR-2003
DEFINITION AR275648
ACCESSION AR275648
VERSION AR275648.1 GI:29709099

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Buell,G.N., Surprenant,A. and Kawashima,E.

TITLE Methods of screening modulators of mammalian P2X7 purinergic receptors
JOURNAL Patent: US 6509163-A 3 21-JAN-2003;
Glaxo Group Limited; Middlesex;
GBX;
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Qy 3 GCGCTATCTGAAG 15
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Db 1 GCGCTATCTGAAG 13
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RESULT 3
BD067608/c
LOCUS BD067608 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067608
VERSION BD067608.1 GI:22613211
KEYWORDS JP 2001511003-A/448.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS 1 (bases 1 to 17)
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 448 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/448
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476, 04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
C12N9/00, C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
CC levels of epidermal growth factor receptors
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Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GTATCTGAAGAGTCTG 21
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Db 16 GTATCGAAGAGTCTG 1
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AR402108/c
LOCUS AR402108 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 448 from patent US 6623962.
ACCESSION AR402108

VERSION AR402108.1 GI:40149558
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 17)
TITLE Akhtar, S., Fell, P. and McSwiggen, J. A.
Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 448 23-SEP-2003;
Sirna Therapeutics, Inc. and Aston University; Boulder, CO
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Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GTATCTGAAGAGTCTG 21
|||||
Db 16 GTATCGAAGAGTCTG 1
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RESULT 5
AL7234/c
LOCUS AL7234 20 bp DNA linear PAT 31-MAR-1994
DEFINITION Oligonucleotide 20-mer BB9513 (SEQ ID NO: 134).
ACCESSION AL7234
VERSION AL7234.1 GI:513003
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS 1 (bases 1 to 20)
TITLE STEM CELL INHIBITING PROTEINS
JOURNAL Patent: WO 9313206-A 134 08-JUL-1993;
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Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CTGGCGTATCTGAAGA 16
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Db 17 CTGACGCATCTGAAGA 2
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RESULT 6
AR027617/c
LOCUS AR027617 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 134 from patent US 5856301.
ACCESSION AR027617
VERSION AR027617.1 GI:5938437
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 20)
TITLE Craig, S., Hunter, M. George., Edwards, R. Mark., Czaplowski, L. George.
Stem cell inhibiting proteins
JOURNAL Patent: US 5856301-A 134 05-JAN-1999;
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DEFINITION	RNA Interference Mediated Inhibition of BCL2 Gene Expression Using	
ACCESSION	DD206720	
VERSION	DD206720.1 GI:85643085	
KEYWORDS	JP 2005517452-A/833.	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Beigelman,L. and Mcswiggen,J.	
TITLE	RNA Interference Mediated Inhibition of BCL2 Gene Expression Using	
JOURNAL	Short Interfering Nucleic Acid (siNA)	
COMMENT	Patent: JP 2005517452-A 833 16-JUN-2005; SiRNA Therapeutics Inc	
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PF	16-JUN-2005	
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18-JUL-2002 US	60/396905,06-JUN-2002 US 60/386782, PR	
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KEYWORDS	JP 2005517452-A/833.	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Beigelman,L. and Mcswiggen,J.	
TITLE	RNA Interference Mediated Inhibition of BCL2 Gene Expression Using	
JOURNAL	Short Interfering Nucleic Acid (siNA)	
COMMENT	Patent: JP 2005517452-A 833 16-JUN-2005; SiRNA Therapeutics Inc	
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PN	JP 2005517452-A/833	
PF	16-JUN-2005	
PR	18-FEB-2003 JP 2003569860	
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VERSION	DD206728.1 GI:85643093	
KEYWORDS	JP 2005517452-A/841.	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Beigelman,L. and Mcswiggen,J.	
TITLE	RNA Interference Mediated Inhibition of BCL2 Gene Expression Using	
JOURNAL	Short Interfering Nucleic Acid (siNA)	
COMMENT	Patent: JP 2005517452-A 841 16-JUN-2005; SiRNA Therapeutics Inc	
OS	Artificial Sequence	
PN	JP 2005517452-A/841	
PD	16-JUN-2005	
PF	18-FEB-2003 JP 2003569860	
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beigelman,james mcswiggen		
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ACCESSION	DD206724	
VERSION	DD206724.1 GI:85643089	
KEYWORDS	JP 2005517452-A/837.	
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ORGANISM	other sequences; artificial sequences.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Beigelman,L. and Mcswiggen,J.	
TITLE	RNA Interference Mediated Inhibition of BCL2 Gene Expression Using	
JOURNAL	Short Interfering Nucleic Acid (siNA)	
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beigelman,james mcswiggen		
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REFERENCE	1 (bases 1 to 21)	
AUTHORS	Beigelman,L. and Mcswiggen,J.	
TITLE	RNA	

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  Db 4 GTCTCTGAAGACTCTG 19
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ACCESSION
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VERSION
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KEYWORDS
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  Patent: JP 2005517452-A 845 16-JUN-2005;
  SiRNA Therapeutics Inc
ORIGIN
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  RNA Interference Mediated Inhibition of BCL2 Gene Expression Using
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  PF 18-FEB-2003 JP 2003569860
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RESULT 11
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
  JP 2005517452-A/849.
SOURCE
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REFERENCE
  1 (bases 1 to 21)
  Beigelman,L. and Mcswiggen,J.
  RNA Interference Mediated Inhibition of BCL2 Gene Expression Using
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  Patent: JP 2005517452-A 849 16-JUN-2005;
  SiRNA Therapeutics Inc
ORIGIN
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  Beigelman,L. and Mcswiggen,J.
  RNA Interference Mediated Inhibition of BCL2 Gene Expression Using
  Short Interfering Nucleic Acid (siNA)
  Patent: JP 2005517452-A 849 16-JUN-2005;
  SiRNA Therapeutics Inc
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  PN JP 2005517452-A/849
  PD 16-JUN-2005
  PF 18-FEB-2003 JP 2003569860
  PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR
  05-SEP-2002 US 60/408378,29-AUG-2002 US 60/406784, PR
  18-JUL-2002 US 60/396905,06-JUN-2002 US 60/386782, PR
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DEFINITION
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ACCESSION
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VERSION DD206740.1 GI:85643105
KEYWORDS JP 2005517452-A/853.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Beigelman,L. and Mcswiggen,J.
TITLE RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA)
JOURNAL Patent: JP 2005517452-A 853 16-JUN-2005;
        Sirna Therapeutics Inc
COMMENT OS Artificial Sequence
        PN JP 2005517452-A/853
        PP 18-FEB-2003 JP 2003569860
        PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR
        OS-SEP-2002 US 60/408378,29-AUG-2002 US 60/406784, PR
        18-JUL-2002 US 60/396905,06-JUN-2002 US 60/386782, PR
        11-MAR-2002 US 60/363124,20-FEB-2002 US 60/358580 PI leonid
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        KEYWORDS JP 2005518803-A/256.
        SOURCE synthetic construct
        ORGANISM other sequences; artificial sequences.
        REFERENCE 1 (bases 1 to 21)
        AUTHORS Jamison,S., Fosunafu,C., Beigelman,L., Chourira,B., Thompson,J.,
        Asuman,N., Pavco,P. and Mcswiggen,J.
        TITLE RNA Interference Mediated Inhibition of Gene Expression Using Short Interfering Nucleic Acid (siNA)
        JOURNAL Patent: JP 2005518803-A 259 30-JUN-2005;
        Sirna Therapeutics Inc
        COMMENT OS Artificial Sequence
        PN JP 2005518803-A/256
        PP 20-FEB-2003 JP 2003573107
        PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR
        OS-SEP-2002 US 60/408378,29-AUG-2002 US 60/406784, PR
        06-JUN-2002 US 60/386782,11-MAR-2002 US 60/363124, PR
        20-FEB-2002 US 60/358580
        PI sharon jamison,cathy fosunafu,leonid beigelman,baratto PI
        chourira,
        PI james thompson,nashimu asuman,pamela pavco,james mcswiggen CC
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        DEFINITION RNA Interference Mediated Inhibition of Gene Expression Using Short Interfering Nucleic Acid (siNA).
        ACCESSION DD207470
        VERSION DD207470.1 GI:85645380
        KEYWORDS JP 2005518803-A/259.
        SOURCE synthetic construct
        ORGANISM other sequences; artificial sequences.
        REFERENCE 1 (bases 1 to 21)
        AUTHORS Jamison,S., Fosunafu,C., Beigelman,L., Chourira,B., Thompson,J.,
        Asuman,N., Favco,P. and Mcswiggen,J.
        TITLE RNA Interference Mediated Inhibition of Gene Expression Using Short Interfering Nucleic Acid (siNA)
        JOURNAL Patent: JP 2005518803-A 259 30-JUN-2005;
        Sirna Therapeutics Inc
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        PN JP 2005518803-A/259
        PP 20-FEB-2003 JP 2003573107
        PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR
        OS-SEP-2002 US 60/408378,29-AUG-2002 US 60/406784, PR
        06-JUN-2002 US 60/386782,11-MAR-2002 US 60/363124, PR
        20-FEB-2002 US 60/358580
        PI sharon jamison,cathy fosunafu,leonid beigelman,baratto PI
        chourira,

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Search completed: June 8, 2006, 23:38:04
Job time : 2003 secs

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Location/Qualifiers
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ORIGIN
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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6 GTATCTGAAGAGTCTG 21
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16 GTCTCTGAAGACTCTG 1

DD207473 21 bp RNA linear PAT 19-JAN-2006
RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA).

DD207473
DD207473.1 GI:85645383
JP 2005518803-A/262.
synthetic construct
synthetic construct
other sequences; artificial
sequences.
1 (bases 1 to 21)
Jamison, S., Founafu, C., Beigelman, L.,
Asuman, N., Pavco, P. and McSwiggen, J.
RNA Interference Mediated Inhibition of Gene
Expression Using Short
Interfering Nucleic Acid (siNA)
Patent: JP 2005518803-A 262 30-JUN-2005;

OS	Artificial Sequence				
PN	JP 2005518803-A/262				
PD	30-JUN-2005				
PP	20-FEB-2003 JP 2003573107				
PR	15-JAN-2003 US 60/440139, 09-SEP-2002 US 60/409293, PR				
05-SEP-2002 US 60/409378, 29-AUG-2002 US 60/406784, PR					
06-JUN-2002 US 60/386782, 11-MAR-2002 US 60/363124, PR					
20-FEB-2002 US 60/358580					
PI	sharon jamison, cathy fosunafu, leonid beigelman, baratto pi				
	chourira,				
PI	james thompson, nashimu asuman, pamela pavco, james mcswiggen CC				
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 23:04:50 ; Search time 2506 seconds
(without alignments)
468.598 Million cell updates/sec

Title: US-09-743-825-8

Perfect score: 21

Sequence: 1 ctggcgatctgaagagctcg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 18086

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_hic:*
- 7: gb_est2:*
- 8: gb_est7:*
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- 10: gb_est9:*
- 11: gb_ges1:*
- 12: gb_ges2:*
- 13: gb_ges3:*
- 14: gb_ges4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	10.2	48.6	15	14	AJ592729
3	10	47.6	21	4	CA851013
4	9.8	46.7	19	11	AZ495849
5	9.8	46.7	19	11	AZ495849
6	9.8	46.7	20	13	AZ282704
7	9.8	46.7	20	14	DU831624
8	9.6	45.7	20	11	AZ489135
9	9.4	44.8	17	13	CL681189
10	9.2	43.8	20	11	AZ316351
11	9.2	43.8	20	11	AZ316351
12	9.2	43.8	20	11	AZ328275
13	9	42.9	10	14	AJ587417
14	9	42.9	16	1	AJ684587
15	9	42.9	18	14	ATH524367
16	9	42.9	20	11	AZ625776
17	9	42.9	21	2	BG924548
18	8.8	41.9	13	14	ATH525876
19	8.8	41.9	17	14	AJ587168

C	21	8.8	41.9	20	4	C00979
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	23	8.8	41.9	20	8	CN497681
C	24	8.6	41.0	19	1	D20709
C	25	8.6	41.0	19	8	AJ671616
C	26	8.6	41.0	20	11	C0778852
C	27	8.6	41.0	20	11	AZ480596
C	28	8.6	41.0	20	11	AZ658035
	29	8.6	41.0	21	13	AG194535
C	30	8.4	40.0	19	11	CW986631
C	31	8.4	40.0	19	14	AZ623493
	32	8.4	40.0	20	11	DX035468
C	33	8.4	40.0	20	11	AZ818271
	34	8.4	40.0	20	14	AG199044
C	35	8.4	40.0	20	14	AG203835
	36	8.4	40.0	21	11	AZ787920
C	37	8.4	40.0	21	14	DU831454
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ALIGNMENTS

RESULT 1
AZ784664

LOCUS

DEFINITION

AZ784664 20 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0027110 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

location/Qualifiers

1. .20

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/clones="UUGC2M0027110"

/sex="Male"

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 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.5%; Score 10.4; DB 11; Length 20;
 Best Local Similarity 91.7%; Pred. No. 2.7e+06;
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Qy 10 CTGAAGAGCTCTG 21
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 Db 1 CTGAAGGCTCTG 12

RESULT 2

AJ592729/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 631B09, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS GSS; right border; T-DNA flanking sequence.

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M., and Leclercq, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

2 (bases 1 to 15)

Balzerque, S.

Direct Submission

Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

FEATURES

source

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 /note="T-DNA flanking sequence
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misc_feature

ORIGIN

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Qy 2 TGGCGTATCTGAAGA 16
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Db 15 TGGAGAACTCGAGA 1

RESULT 3

CA851013/c

LOCUS

DEFINITION D09B11_C11_04.abi cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D09B11 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

AUTHORS

TITLE

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

JOURNAL

PUBMED

COMMENT

Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
 Tel: 301 504 5750
 Fax: 301 504 5728
 Email: alkharouf@ba.ars.usda.gov.

FEATURES

source

1. 21
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 /note="Vector: pBluescript SK-; cDNA clones from mRNA
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Db 20 GCGTATCTGATATTATG 3

RESULT 4

AZ495849/c

LOCUS

DEFINITION LM0331N22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

19 bp DNA linear GSS 05-OCT-2000

clone UUGC1M0331N22 R, genomic survey sequence.		clone UUGC2M0190A02 R, genomic survey sequence.	
ACCESSION	AZ495849	ACCESSION	AZ875769
VERSION	AZ495849.1	VERSION	AZ875769.1
KEYWORDS	GI:10671571	KEYWORDS	GI:13086107
SOURCE	GSS.	SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)	ORGANISM	Mus musculus (house mouse)
REFERENCE		REFERENCE	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 19)	AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 19)
TITLE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	TITLE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)	JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0331 row: N column: 22 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.	COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0190 row: A column: 02 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.
FEATURES	Location/Qualifiers 1..19 /organism="Mus musculus" /mol_type="Genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0331N22" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	FEATURES	Location/Qualifiers 1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0190A02" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN		ORIGIN	
Query Match	46.7%; Score 9.8; DB 11; Length 19;	Query Match	46.7%; Score 9.8; DB 11; Length 19;
Best Local Similarity	84.6%; Pred. NO. 5.4e+06;	Best Local Similarity	84.6%; Pred. NO. 5.4e+06;
Matches	11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches	11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	9 TCTGAAGAGTCTG 21 	Qy	1 CTGGCGTATCTGA 13
Db	15 TCTGCAGAGCCTG 3 	Db	7 CTGGAGTGTCTGA 19
RESULT 5		RESULT 6	
AZ875769		CZ282704	
LOCUS	AZ875769 19 bp DNA linear GSS 21-FEB-2001		

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LOCUS      CZ282704      20 bp      DNA      linear      GSS 01-JUL-2005
DEFINITION parapsilosis Candida parapsilosis Random Genomic Library Candida
ACCESSION  CZ282704
VERSION    CZ282704.1  GI:68453906
KEYWORDS   GSS.
SOURCE     Candida parapsilosis
ORGANISM   Candida parapsilosis
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitoporic Saccharomycetales; Candida.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Logue,M.E., Wong,S., Wolfe,K.H. and Butler,G.
TITLE     A genome sequence survey shows that the pathogenic yeast Candida
          parapsilosis has a defective MTL1 allele at its mating type locus
JOURNAL   Eukaryot. Cell 4 (6), 1009-1017 (2005)
PUBMED    15947193
COMMENT    Department of Biochemistry, Conway Institute of Biomolecular and
            Biomedical Research
            University College Dublin
            Dublin 4, Ireland
            Tel: +353 1 7166885
            Fax: +353 1 2837211
            Email: mary.e.logue@ucd.ie
            Class: plasmid ends.
FEATURES   source
            1..20
            Location/Qualifiers
                /organism="Candida parapsilosis"
                /mol_type="genomic DNA"
                /strain="ClIB214"
                /db_xref="taxon:5480"
                /clone="cp25h01"
                /clone_lib="Candida parapsilosis Random Genomic Library"
ORIGIN
Query Match      46.7%; Score 9.8; DB 13; Length 20;
Best Local Similarity 84.6%; Pred. No. 5.4e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TGGCGTATCTGAA 14
        |||||||
Db      6 TGACGTATTGAA 18

RESULT 7
DU831624
LOCUS      DU831624      20 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBrS008M03F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS008M03, genomic survey
            sequence.
ACCESSION  DU831624
VERSION    DU831624.1  GI:83868220
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
            1 (bases 1 to 20)
REFERENCE  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
            End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
            Unpublished (2005)
            Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbcom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS008M03

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Seq primer: T7
Class: BAC ends.
FEATURES   source
            1..20
            Location/Qualifiers
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                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS008M03"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAS."
ORIGIN
Query Match      46.7%; Score 9.8; DB 14; Length 20;
Best Local Similarity 84.6%; Pred. No. 5.4e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 TCTGAAGAGTCTG 21
        |||||||
Db      2 TTTGAAGAGTTTG 14

RESULT 8
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LOCUS      AZ489135      20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION 1M0319H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0319H15 R, genomic survey sequence.
ACCESSION  AZ489135
VERSION    AZ489135.1  GI:10658589
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
            1 (bases 1 to 20)
REFERENCE  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dduun@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0319 row: H column: 15
            Seq primer: CACACAGGAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers
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                /db_xref="taxon:10090"
                /clone="UUGC1M0319H15"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource

```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.7%; Score 9.6; DB 11; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.8e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGGCGTATCTGAAGAG 17
|||||
Db 3 TGGCTTTCTGAGGG 18

RESULT 9

CL681189
LOCUS
DEFINITION
CL681189.1 GI:50188197
pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

CL681189
PRI0130b.G06.2 - PRI0130b.BR (17) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
CL681189.1 GI:50188197
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
1 (bases 1 to 17)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES

source

1..17
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 44.8%; Score 9.4; DB 13; Length 17;
Best Local Similarity 90.9%; Pred. No. 8.4e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 GTATCTGAAGA 16

Db

RESULT 10

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM001K17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 11; Length 20;
Best Local Similarity 78.6%; Pred. No. 1.1e+07;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

|||||
6 GTATCTGCAGA 16

AZ308384
1M0011K17F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM001K17 F, genomic survey sequence.

AZ308384
A2308384.1 GI:10348326

GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: K column: 17
Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends
High quality sequence stop: 20.

Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGCLM001K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-

/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

QY 8 ATCTGAAGAGTCTG 21
 |||||
 Db 4 ATCTGAAGTGACCG 17

RESULT 11
 AZ316351/c
 LOCUS
 DEFINITION 1M0034A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0034A11 F, genomic survey sequence.

ACCESSION AZ316351
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0034 row: A column: 11
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 Location/Qualifiers
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/organism="Mus musculus"
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 /strain="C57BL/6J"
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 /clone="UUGC1M0034A11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 11; Length 20;
 Best Local Similarity 78.6%; Pred. No. 1.1e+07;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 ATCTGAAGAGTCTG 21
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 Db 20 ATCTCAAGATACTG 7

RESULT 12
 AZ328275/c
 LOCUS

DEFINITION 1M0052A01F Mouse 20 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0052A01 F, genomic survey sequence.

ACCESSION AZ328275
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0052 row: A column: 01
 Seg primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0052A01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 11; Length 20;
 Best Local Similarity 78.6%; Pred. No. 1.1e+07;

to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobio.gen.fr/>).

FEATURES

source

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1..18
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ORIGIN

Query Match 42.9%; Score 9; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ATCTGAGA 16
 |||||
 Db 5 ATCTGAGA 13

Search completed: June 9, 2006, 00:19:59
 Job time : 2510 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 23:38:20 ; Search time 100 Seconds
(without alignments)
392.933 Million cell updates/sec

Title: US-09-743-825-8

Perfect score: 21

Sequence: 1 ctggcgatctgaagagctctg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 538872

Minimum DB seq length: 0

Maximum DB seq length: 21

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Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
- 8: /EMC Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfileseq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	61.9	20	3	US-08-842-079-3
2	13	61.9	20	3	US-09-638-857-3
C 3	12.8	61.0	17	3	US-08-985-162-448
C 4	12.8	61.0	17	3	US-09-401-063-448
C 5	12.8	61.0	20	2	US-08-450-905B-134
C 6	12.8	61.0	20	3	US-07-982-759F-134
C 7	12.2	58.1	17	3	US-08-985-162-449
C 8	12.2	58.1	17	3	US-09-401-063-449
9	12.2	58.1	20	2	US-08-717-291-8
10	12.2	58.1	20	3	US-08-728-603-8
C 11	12	57.1	20	3	US-09-433-699-73
C 12	11.8	56.2	16	3	US-09-371-772B-5737
C 13	11.8	56.2	16	5	US-10-138-674B-5737
14	11.8	56.2	17	2	US-07-852-260-4
15	11.8	56.2	17	2	US-07-936-421-18
16	11.8	56.2	17	3	US-08-461-503-4
C 17	11.8	56.2	17	3	US-08-985-162-447
C 18	11.8	56.2	17	3	US-08-465-250-4
19	11.8	56.2	17	3	US-09-371-772B-4438
C 20	11.8	56.2	17	3	US-09-401-063-447
21	11.8	56.2	17	5	US-10-138-674B-4438
22	11.8	56.2	17	5	US-10-138-674B-7389
C 23	11.8	56.2	20	3	US-09-488-671B-38

C 24	11.8	56.2	20	3	US-09-198-452A-1366
C 25	11.8	56.2	21	3	US-09-478-189-118
26	11.6	55.2	20	3	US-09-280-805-129
27	11.6	55.2	20	3	US-09-517-467B-30
C 28	11.6	55.2	20	3	US-09-198-452A-2767
C 29	11.6	55.2	20	3	US-09-657-289A-12
C 30	11.6	55.2	20	3	US-10-130-158A-12
C 31	11.6	55.2	21	3	US-09-657-472-1916
C 32	11.4	54.3	19	3	US-08-422-978-6486
C 33	11.4	54.3	20	2	US-08-602-093-12
C 34	11.4	54.3	20	3	US-09-906-158-68
C 35	11.4	54.3	20	3	US-10-002-623-930
C 36	11.2	53.3	17	3	US-08-985-162-450
C 37	11.2	53.3	17	3	US-09-401-063-450
38	11.2	53.3	17	5	US-10-156-306B-4879
39	11.2	53.3	18	3	US-09-422-978-5682
40	11.2	53.3	19	2	US-08-555-678-57
C 41	11.2	53.3	19	3	US-09-422-978-4659
C 42	11.2	53.3	19	3	US-09-696-791-466
C 43	11.2	53.3	19	3	US-09-696-791-467
44	11.2	53.3	20	3	US-09-488-671-22
45	11.2	53.3	20	3	US-09-488-671-23

ALIGNMENTS

RESULT 1
US-08-842-079-3
; Sequence 3, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-842-079-3

Query Match 61.9%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 GGCCTATCTGAAG 15
Db 1 GGCCTATCTGAAG 13
|||||

RESULT 2
US-09-638-857-3
; Sequence 3, Application US/09638857
; Patent No. 6509163
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/09/638,857
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 08/842,079
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-638-857-3

Query Match 61.9%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGTATCTGAAG 15
Db 1 GCGTATCTGAAG 13

RESULT 3
US-08-985-162-448/c
; Sequence 448, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 448:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-985-162-448
Query Match 61.0%; Score 12.8; DB 3; Length 17;
Best Local Similarity 87.5%; Pred.No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21

Db 16 GTATCGAAGAGTCTG 1

RESULT 4
US-09-401-063-448/c
; Sequence 448, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 448:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-401-063-448
Query Match 61.0%; Score 12.8; DB 3; Length 17;
Best Local Similarity 87.5%; Pred.No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21

Db 16 GTATCGAAGAGTCTG 1

RESULT 5
US-08-450-905B-134/c
; Sequence 134, Application US/08450905B
; Patent No. 5856301
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Stem Cell Inhibiting Proteins
; NUMBER OF SEQUENCES: 178

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HALE and DORR
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: MA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: 26-MAR-1995
;; APPLICATION NUMBER: US/08/450,905B
;; PRIOR APPLICATION DATA:
;; FILING DATE: 07/982,759
;; APPLICATION NUMBER: 07/982,759
;; FILING DATE: 08-MAR-1993
;; PRIOR APPLICATION DATA:
;; FILING DATE: 23-DEC-1991
;; APPLICATION NUMBER: GB 9127319.3
;; FILING DATE: 14-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BAKER, HOLLIE L.
;; REGISTRATION NUMBER: 31,321
;; REFERENCE/DOCKET NUMBER: 102.378.120DV-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-526-6110
;; TELEFAX: 617-526-5000
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..20
;; OTHER INFORMATION: /product= "BB9513 oligomer"
US-08-450-905B-134

Query Match 61.0%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGTATCTGAAGA 16
Db 17 CTGAGCGATCTGAAGA 2

RESULT 6
US-07-982-759F-134/c
; Sequence 134, Application US/07982759F
; Patent No. 6057123
; GENERAL INFORMATION:
; APPLICANT: CRAIG, Stewart
; APPLICANT: GEORGE, Michael
; APPLICANT: EDWARDS, Richard Mark
; APPLICANT: CZAPLEWSKI, Lloyd George
; APPLICANT: GILBERT, Richard
; TITLE OF INVENTION: Stem Cell Inhibiting Proteins
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/982,759F
;; FILING DATE: 08-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9127319.3
;; FILING DATE: 23-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9221587.0
;; FILING DATE: 14-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BAKER, HOLLIE L.
;; REGISTRATION NUMBER: 31,321
;; REFERENCE/DOCKET NUMBER: 102378.120
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-526-6000
;; TELEFAX: 617-526-5000
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..20
;; OTHER INFORMATION: /product= "BB9513 oligomer"
US-07-982-759F-134

Query Match 61.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGTATCTGAAGA 16
Db 17 CTGAGCGATCTGAAGA 2

RESULT 7
US-08-985-162-449/c
; Sequence 449, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476

; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 449:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-449

Query Match 58.1%; Score 12.2; DB 3; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGTATCTGAAGAGTCT 20
| | | | | | | | | | | | | | | | | |
Db 17 GGGTATCGAAAGAGTCT 1

RESULT 8
US-09-401-063-449/c
; Sequence 449, Application US/09401063
; Patent No. 662362
; GENERAL INFORMATION:

; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 449:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-401-063-449

Query Match 58.1%; Score 12.2; DB 3; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGTATCTGAAGAGTCT 20
| | | | | | | | | | | | | | | | | |
Db 17 GGGTATCGAAAGAGTCT 1

RESULT 9
US-08-717-291-8
; Sequence 8, Application US/08717291
; Patent No. 5908773
; GENERAL INFORMATION:
; APPLICANT: Cesarman, Ethel
; APPLICANT: Arvanitakis, Leandros
; APPLICANT: Knowles, Daniel M.
; APPLICANT: Mesri, Enrique
; TITLE OF INVENTION: KSHV POSITIVE CELL LINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,291
; FILING DATE:

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/1360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-717-291-8

Query Match 58.1%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 9.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CGGTATCTGAAGAGTCTG 21
| | | | | | | | | | | | | | | | | |
Db 1 CGGAGCTAAGAGTCTG 17

RESULT 10
US-08-728-603-8
; Sequence 8, Application US/08728603
; Patent No. 6093806
; GENERAL INFORMATION:
; APPLICANT: Cesarman, Ethel
; APPLICANT: Knowles, Daniel M.


```

; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/852,260
; FILING DATE: 19920619
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-07-852-260-4

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Query Match 56.2%; Score 11.8; DB 2; Length 17;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 3 GCGGTATCTGAAGAG 17
Db 1 GCGGTATCTGAAG 15

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RESULT 15
US-07-936-421-18
; Sequence 18, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

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; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/936,421
; FILING DATE: 19920826
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-936-421-18

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Query Match 56.2%; Score 11.8; DB 2; Length 17;
Best Local Similarity 53.3%; Pred. No. 1.4e+04;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Oy 6 GTATCTGAAGAGTCT 20
Db 3 GUCUCUGAGACUCU 17

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Search completed: June 9, 2006, 00:21:43
Job time : 102 secs

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1	14.4	68.6	19	14	US-11-083-784-277064	Sequence 277064,
2	14.4	68.6	19	15	US-11-101-244-277064	Sequence 277064,
3	14.4	68.6	20	11	US-10-310-914A-1347779	Sequence 1347779,
C	14.2	67.6	19	11	US-10-310-914A-1368338	Sequence 1368338,
C	14.2	67.6	19	14	US-11-083-784-252899	Sequence 252899,
5	14.2	67.6	19	14	US-11-083-784-880853	Sequence 880853,
6	14.2	67.6	19	14	US-11-083-784-880956	Sequence 880956,
7	14.2	67.6	19	14	US-11-083-784-1324693	Sequence 1324693,
8	14.2	67.6	19	14	US-11-083-784-880956	Sequence 880956,
9	14.2	67.6	19	15	US-11-101-244-252899	Sequence 252899,
10	14.2	67.6	19	15	US-11-101-244-880853	Sequence 880853,
11	14.2	67.6	19	15	US-11-101-244-880956	Sequence 880956,
12	14.2	67.6	19	15	US-11-101-244-1324693	Sequence 1324693,
13	13.8	65.7	19	14	US-11-083-784-346041	Sequence 346041,
14	13.8	65.7	19	15	US-11-083-784-346141	Sequence 346141,
15	13.8	65.7	19	15	US-11-101-244-346041	Sequence 346041,
16	13.8	65.7	19	15	US-11-101-244-346141	Sequence 346141,
17	13.8	65.7	20	18	US-10-619-739-1019	Sequence 1019, Ap

US-11-101-244-277064

RESULT 2

US-11-101-244-277064

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; Sequence 277064, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 277064
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-277064

Query Match      68.6%; Score 14.4; DB 15; Length 19;
Best Local Similarity 68.8%; Pred. No. 5.1e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CTGGCGTATCTGAAGA 16
Db      4 CUGGCCAUUCUGAAGA 19

RESULT 3
US-10-310-914A-1347779/C
; Sequence 1347779, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwick, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: uses thereof
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1347779
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1347779

Query Match      68.6%; Score 14.4; DB 11; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 GTATCTGAAGAGTCTG 21
Db     18 GGATCTGAAGAGTCTG 3

RESULT 4
US-10-310-914A-1368338/C
; Sequence 1368338, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwick, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: uses thereof
; CURRENT APPLICATION NUMBER: 60/426,137
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

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; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1368338
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1368338

Query Match      67.6%; Score 14.2; DB 11; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GCGGTATCTGAAGAGTCTG 21
Db     19 GGAGAACTGAAGATTCTG 1

RESULT 5
US-11-083-784-252899
; Sequence 252899, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 252899
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-252899

Query Match      67.6%; Score 14.2; DB 14; Length 19;
Best Local Similarity 52.6%; Pred. No. 6.5e+03;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGGGTATCTGAAGAGTCT 20
Db      1 UGACAUUUCUGAAGAGUCU 19

RESULT 6
US-11-083-784-880853
; Sequence 880853, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333

```

```
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 880853
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-880853

Query Match      67.6%; Score 14.2; DB 14; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGCGTATCTGAAGAGTCT 20
   :|||:|||||:|:
Db 1 UGAUGAAUCUGAAGAGUCU 19

RESULT 7
US-11-083-784-880956
; Sequence 880956, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 880956
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-880956

Query Match      67.6%; Score 14.2; DB 14; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGCGTATCTGAAGAGTCT 20
   :|||:|||||:|:
Db 1 UGAUGAAUCUGAAGAGUCU 19

RESULT 8
US-11-083-784-1324693
; Sequence 1324693, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

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; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1324693
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1324693

Query Match      67.6%; Score 14.2; DB 14; Length 19;
Best Local Similarity 52.6%; Pred. No. 6.5e+03;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGCGTATCTGAAGAGTCT 20
   :||||:|:|:|:|:|:
Db 1 UGGCGUAUCUGAACCAUCU 19

RESULT 9
US-11-101-244-252899
; Sequence 252899, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 252899
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-252899

Query Match      67.6%; Score 14.2; DB 15; Length 19;
Best Local Similarity 52.6%; Pred. No. 6.5e+03;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGCGTATCTGAAGAGTCT 20
   :|||:|:|:|:|:|:
Db 1 UGACAUUUCUGAAGAGUCU 19

RESULT 10
US-11-101-244-880853
; Sequence 880853, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 80853
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-880853
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Query Match          67.6%; Score 14.2; DB 15; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY  2 TGGCGTATCTGAAGAGTCT 20
    :|||:|||||:|:
Db   1 UGAUGAUCUGAAGAGUCU 19
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RESULT 11
US-11-101-244-880956
; Sequence 880956, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 880956
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-880956
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Query Match          67.6%; Score 14.2; DB 15; Length 19;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY  2 TGGCGTATCTGAAGAGTCT 20
    :|||:|||||:|:
Db   1 UGAUGAUCUGAAGAGUCU 19
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RESULT 12
US-11-101-244-1324693
; Sequence 1324693, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
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; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1324693
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1324693
```

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Query Match          67.6%; Score 14.2; DB 15; Length 19;
Best Local Similarity 52.6%; Pred. No. 6.5e+03;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY  2 TGGCGTATCTGAAGAGTCT 20
    :|||:|||||:|:
Db   1 UGGCGUAUCUGAACCAUCU 19
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RESULT 13
US-11-083-784-346041
; Sequence 346041, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 346041
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-346041
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Query Match          65.7%; Score 13.8; DB 14; Length 19;
Best Local Similarity 58.8%; Pred. No. 1e+04;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY  2 TGGCGTATCTGAAGAGT 18
    :|||:|||||:|:
Db   1 UUGAGUAUCUGAAGAGU 17
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RESULT 14
US-11-083-784-346141
; Sequence 346141, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 346141
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-346141

Query Match      65.7%; Score 13.8; DB 14; Length 19;
Best Local Similarity 58.8%; Pred. No. 1e+04;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGCGTATCTGAAGAGT 18
DB      1 UUGAGUAUCUGAAGAGU 17

RESULT 15
US-11-101-244-346041
; Sequence 346041, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 346041
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-346041

Query Match      65.7%; Score 13.8; DB 15; Length 19;
Best Local Similarity 58.8%; Pred. No. 1e+04;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 TGGCGTATCTGAAGAGT 18
DB      1 UUGAGUAUCUGAAGAGU 17

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Search completed: June 9, 2006, 00:36:01
Job time : 848 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 00:22:00 ; Search time 25 Seconds
(without alignments)
106.616 Million cell updates/sec

Title: US-09-743-825-8

Perfect score: 21

Sequence: 1 ctggcgatctctgaagagtctg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 20774

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	11.8	56.2	17	6	US-10-514-776-361
2	10.8	51.4	19	6	US-10-994-215-56
3	10.2	48.6	20	6	US-10-511-832-58
4	10.2	48.6	21	6	US-10-539-032-22
5	10.2	48.6	21	7	US-11-251-465-460
6	10	47.6	11	7	US-11-158-209-277
7	10	47.6	19	7	US-11-251-465-137
8	10	47.6	19	7	US-11-251-465-503
9	10	47.6	20	7	US-11-296-092-106
10	10	47.6	21	7	US-11-251-465-240
11	10	47.6	21	7	US-11-251-465-504
12	10	47.6	21	7	US-11-267-943-10
13	10	47.6	21	7	US-11-264-023-10
14	9.8	46.7	18	7	US-11-293-697-5436
15	9.8	46.7	19	7	US-11-283-484A-2
16	9.6	45.7	18	7	US-11-293-697-5003
17	9.4	44.8	19	7	US-11-251-465-587
18	9.4	44.8	20	6	US-10-511-937-2085
19	9.4	44.8	20	6	US-10-511-832-45
20	9.4	44.8	20	7	US-11-204-427-33
21	9.4	44.8	20	7	US-11-204-427-36
22	9.4	44.8	20	7	US-11-204-427-38
23	9.4	44.8	21	7	US-11-251-465-588
24	9.2	43.8	19	7	US-11-251-465-589
25	9.2	43.8	19	7	US-11-251-465-769

26	9.2	43.8	19	7	US-11-267-942-15	Sequence 15, Appl
c 27	9.2	43.8	19	7	US-11-293-697-5255	Sequence 5255, Ap
c 28	9.2	43.8	21	6	US-10-511-937-843	Sequence 843, App
29	9.2	43.8	21	7	US-11-251-465-770	Sequence 770, App
c 30	9.2	43.8	21	7	US-11-235-385-7	Sequence 7, Appl
c 31	9.2	43.8	21	7	US-11-235-385-15	Sequence 15, Appl
c 32	9.2	43.8	21	7	US-11-235-385-21	Sequence 21, Appl
c 33	9.2	43.8	21	7	US-11-235-385-35	Sequence 35, Appl
c 34	9.2	43.8	21	7	US-11-173-889-50	Sequence 50, Appl
c 35	9.2	43.8	21	7	US-11-173-889-66	Sequence 66, Appl
c 36	9	42.9	18	6	US-10-523-356-38	Sequence 38, Appl
37	9	42.9	18	7	US-11-242-111-60	Sequence 60, Appl
38	9	42.9	20	6	US-10-511-937-715	Sequence 715, App
c 39	9	42.9	20	6	US-10-511-937-1168	Sequence 1168, Ap
40	9	42.9	20	6	US-10-511-937-2052	Sequence 2052, Ap
41	9	42.9	20	6	US-10-511-832-35	Sequence 35, Appl
c 42	9	42.9	20	7	US-11-336-198-4	Sequence 4, Appl
43	9	42.9	21	7	US-11-242-139-116	Sequence 116, App
44	8.8	41.9	17	6	US-10-514-776-355	Sequence 355, App
45	8.8	41.9	17	6	US-10-514-776-360	Sequence 360, App

ALIGNMENTS

RESULT 1
US-10-514-776-361
; Sequence 361, Application US/10514776
; Publication No. US20060094008A1
; GENERAL INFORMATION:
; APPLICANT: Symex Corporation
; TITLE OF INVENTION: CK primer
; FILE REFERENCE: GP03-1006PCT
; CURRENT APPLICATION NUMBER: US/10/514,776
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: JP P2002-145689
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: JP P2002-175271
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP P2002-199759
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 361
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed DNA based on CK19 gene
US-10-514-776-361

Query Match 56.2%; Score 11.8; DB 6; Length 17;
Best Local Similarity 86.7%; Pred No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGTATCTGAAG 15
||| |||||
Db 3 CTGGCCTACTGAAG 17

RESULT 2
US-10-994-215-56
; Sequence 56, Application US/10994215
; Publication No. US20060111302A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO REDUCE MUTAGENESIS
; FILE REFERENCE: 91-000110US
; CURRENT APPLICATION NUMBER: US/10/994,215
; CURRENT FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 56

; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: synthetic oligonucleotide primer
 US-10-994-215-56

Query Match 51.4%; Score 10.8; DB 6; Length 19;
 Best Local Similarity 85.7%; Pred. No. 2.3e+03;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGCGTATCTGAAG 15
 Db 3 TGGCGTATCTGAAG 16

RESULT 3

US-10-511-832-58/c
 ; Sequence 58, Application US/10511832
 ; Publication No. US20060105973A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan M. Freier
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTEROID
 ; TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION
 ; FILE REFERENCE: RTS-0428
 ; CURRENT APPLICATION NUMBER: US/10/511,832
 ; CURRENT FILING DATE: 2004-10-19
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 58
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-511-832-58

Query Match 48.6%; Score 10.2; DB 6; Length 20;
 Best Local Similarity 80.0%; Pred. No. 4.8e+03;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CGTATCTGAAGATC 19
 Db 15 CTTATCTGAAGCCTC 1

RESULT 4

US-10-539-032-22
 ; Sequence 22, Application US/10539032
 ; Publication No. US20060116505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY AGENCY
 ; TITLE OF INVENTION: Glucose and/or fructose transporter 'NaGLT1' and gene thereof
 ; FILE REFERENCE: 4439-4034
 ; CURRENT APPLICATION NUMBER: US/10/539,032
 ; CURRENT FILING DATE: 2005-06-13
 ; PRIOR APPLICATION NUMBER: JP P2002-363014
 ; PRIOR FILING DATE: 2002-12-13
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NaGLT1 reverse
 ; OTHER INFORMATION: primer
 US-10-539-032-22

Query Match 48.6%; Score 10.2; DB 6; Length 21;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGTATCTGAAGAG 17
 Db 7 GCGGAACACTGAAGTG 21

RESULT 5

US-11-251-465-460/c
 ; Sequence 460, Application US/11251465
 ; Publication No. US20060094061A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brys, Reginald
 ; APPLICANT: Vandeghinste, Nick
 ; APPLICANT: Tomme, Peter
 ; APPLICANT: Klaassen, Hubertus
 ; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
 ; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
 ; TITLE OF INVENTION: Inflammatory Diseases
 ; FILE REFERENCE: P30,172-A USA
 ; CURRENT APPLICATION NUMBER: US/11/251,465
 ; CURRENT FILING DATE: 2005-10-14
 ; PRIOR APPLICATION NUMBER: 60/619,384
 ; PRIOR FILING DATE: 2004-10-15
 ; NUMBER OF SEQ ID NOS: 880
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 460
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Knock-down target sequence
 US-11-251-465-460

Query Match 48.6%; Score 10.2; DB 7; Length 21;
 Best Local Similarity 80.0%; Pred. No. 4.9e+03;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TATCTGAAGATCTCTG 21
 Db 16 TTCTCTGCAGATCTCTG 2

RESULT 6

US-11-158-209-277/c
 ; Sequence 277, Application US/11158209
 ; Publication No. US2006008852A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dirk Petersohn
 ; APPLICANT: Kordula Schlotmann
 ; APPLICANT: Thomas Gassenmeier
 ; APPLICANT: Olaf Holtkotter
 ; APPLICANT: Marcus Conradt
 ; APPLICANT: Kay Hofmann
 ; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
 ; FILE REFERENCE: H 05667 PCT
 ; CURRENT APPLICATION NUMBER: US/11/158,209
 ; CURRENT FILING DATE: 2005-06-20
 ; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
 ; PRIOR FILING DATE: 2003-12-11
 ; PRIOR APPLICATION NUMBER: 102 60 931.4-41
 ; PRIOR FILING DATE: 2002-12-20
 ; NUMBER OF SEQ ID NOS: 1335
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 277
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-158-209-277

Query Match 47.6%; Score 10; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CTGAAGAGTC 19

```
Db      10  CTGAAGAGTC 1
|||||
RESULT 7
US-11-251-465-137/c
; Sequence 137, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 137
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-137
Query Match      47.6%; Score 10; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  GAAGAGTCTG 21
|||||
Db      19  GAAGAGTCTG 10
|||||

RESULT 8
US-11-251-465-503
; Sequence 503, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 503
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-503
Query Match      47.6%; Score 10; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  GAAGAGTCTG 21
|||||
```

```
Db      3  GAAGAGTCTG 12
|||||
RESULT 9
US-11-296-092-106
; Sequence 106, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-11-296-092-106
Query Match      47.6%; Score 10; DB 7; Length 20;
Best Local Similarity 72.2%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  TGGCGTATCTGAAGAGTC 19
|||||
Db      1  TGGCCAGCTGACGAGCC 18
|||||

RESULT 10
US-11-251-465-240/c
; Sequence 240, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 240
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-240

Query Match          47.6%; Score 10; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAAGAGTCTG 21
    |||||
Db 21 GAAGAGTCTG 12

RESULT 11
US-11-251-465-504
; Sequence 504, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; PRIOR FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 504
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-504

Query Match          47.6%; Score 10; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAAGAGTCTG 21
    |||||
Db 5 GAAGAGTCTG 14

RESULT 12
US-11-267-942-10/c
; Sequence 10, Application US/11267942
; Publication No. US20060094054A1
; GENERAL INFORMATION:
; APPLICANT: Schiemann, William P.
```

```
; APPLICANT: Albig, Allan R.
; TITLE OF INVENTION: Fibulin-3 and Uses Thereof
; FILE REFERENCE: 2879-109
; CURRENT APPLICATION NUMBER: US/11/267,942
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 60/625,598
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/687,129
; PRIOR FILING DATE: 2005-06-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-11-267-942-10

Query Match          47.6%; Score 10; DB 7; Length 21;
Best Local Similarity 72.2%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GCGTATCTGAAGAGTCT 20
    |||||
Db 19 GGCATATCCACAGAGGCT 2

RESULT 13
US-11-264-029-10
; Sequence 10, Application US/11264029
; Publication No. US20060099171A1
; GENERAL INFORMATION:
; APPLICANT: University of Pennsylvania
; TITLE OF INVENTION: mGIRL IS COSTIMULATORY FOR T CELLS
; FILE REFERENCE: P-8296-US
; CURRENT APPLICATION NUMBER: US/11/264,029
; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer
US-11-264-029-10

Query Match          47.6%; Score 10; DB 7; Length 21;
Best Local Similarity 72.2%; Pred. No. 6.2e+03;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GCGTATCTGAAGAGTCTG 21
    |||||
Db 4 GCGAAGCTGAAGATACTG 21

RESULT 14
US-11-293-697-5436
; Sequence 5436, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5436
; LENGTH: 18
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-11-293-697-5436

Query Match          46.7%; Score 9.8; DB 7; Length 18;
Best Local Similarity 84.6%; Pred. No. 7.7e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCTGAAGAGTCTG 21
   |||||
DB 3 TGTGAAGAGCCTG 15

RESULT 15
US-11-283-484A-2
; Sequence 2, Application US/11283484A
; Publication No. US20060115461A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Robertson, Barbara
; APPLICANT: Leake, Devin
; APPLICANT: Robinson, Kathryn
; APPLICANT: Marshall, William S.
; APPLICANT: Khvorova, Anastasia S.
; TITLE OF INVENTION: APPARATUS AND SYSTEM HAVING DRY GENE SILENCING COMPOSITIONS
; FILE REFERENCE: Attorney Docket No. 16542.1
; CURRENT APPLICATION NUMBER: US/11/283,484A
; PRIOR FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/630320
; PRIOR FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/678165
; PRIOR FILING DATE: 2005-05-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: siRNA targeting a SRD5a1 gene
US-11-283-484A-2

Query Match          46.7%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 7.7e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATCTGAAGAGTCT 20
   |||||
DB 7 ATTTGAAGAGTAT 19

Search completed: June 9, 2006, 00:36:32
Job time : 25 secs
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 00:36:46 ; Search time 1983 Seconds
(without alignments)
644.956 Million cell updates/sec

Title: US-09-743-825-10

Perfect score: 20

Sequence: 1 gaccgcataagacttctcaga 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1002524

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vl.*

11: gb_ov.*

12: gb_htg.*

13: gb_in.*

14: gb_on.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	69.0	20	2	AR312275 Sequence
2	13.2	66.0	20	2	AR614263 Sequence
3	12.6	63.0	20	2	AR633611 Sequence
4	12.2	61.0	18	2	AR096404 Sequence
5	12.2	61.0	18	2	BD217452 Antisense
6	12.2	61.0	20	2	AR633610 Sequence
7	12	60.0	20	2	AR031072 Sequence
8	12	60.0	20	2	AR152833 Sequence
9	12	60.0	20	2	BD134289 Detection
10	11.8	59.0	17	2	AX735344 Sequence
11	11.8	59.0	17	2	AX759065 Sequence
12	11.8	59.0	18	2	A65727 Sequence 8
13	11.8	59.0	18	2	AR048183 Sequence
14	11.8	59.0	18	2	E10136 PCR primer
15	11.8	59.0	19	2	DD200317 RNA Inter
16	11.8	59.0	19	2	DD200470 RNA Inter
17	11.8	59.0	20	2	AR023697 Sequence
18	11.6	58.0	19	2	CS014609 Sequence

c	19	11.6	58.0	19	2	CS015023 Sequence
	20	11.6	58.0	19	2	AX207008 Sequence
	21	11.6	58.0	20	2	AR637111 Sequence
	22	11.6	58.0	20	2	AX353519 Sequence
	23	11.4	57.0	15	2	CS005340 Sequence
	24	11.4	57.0	15	2	I61735 Sequence 28
	25	11.4	57.0	15	2	AX636229 Sequence
	26	11.4	57.0	17	2	AR111392 Sequence
	27	11.4	57.0	17	2	AR364674 Sequence
	28	11.4	57.0	17	2	AX734698 Sequence
	29	11.4	57.0	19	2	AR571910 Sequence
	30	11.4	57.0	19	2	AR571911 Sequence
	31	11.4	57.0	19	2	AX130020 Sequence
	32	11.4	57.0	19	2	AX130021 Sequence
	33	11.4	57.0	20	2	AR569156 Sequence
	34	11.4	57.0	20	2	AR569157 Sequence
	35	11.4	57.0	20	2	AX269412 Sequence
	36	11.4	57.0	20	2	AX270943 Sequence
	37	11.2	56.0	18	2	AR292962 Sequence
	38	11.2	56.0	19	2	AX378663 Sequence
	39	11.2	56.0	20	2	AR072310 Sequence
	40	11.2	56.0	20	2	AR123092 Sequence
	41	11.2	56.0	20	2	C0770343 Sequence
	42	11.2	56.0	20	2	C0898991 Sequence
	43	11.2	56.0	20	2	C0889953 Sequence
	44	11.2	56.0	20	2	I26421 Sequence 11
	45	11.2	56.0	20	2	AR313207 Sequence

ALIGNMENTS

RESULT 1	AR312275	Sequence 2812 from patent US 6559294.	20 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	AR312275					
DEFINITION	AR312275					
ACCESSION	AR312275.1	GI:31705701				
VERSION	AR312275.1					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Griffais, R., Hoise, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.					
TITLE	Chlamydia pneumoniae polynucleotides and uses thereof					
JOURNAL	Patent: US 6559294-A 2812 06-MAY-2003;					
	Genset, S.A.;					
FRATRES	FRX;					
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LOCUS	AR614263					
DEFINITION	AR614263					
ACCESSION	AR614263					
VERSION	AR614263.1	GI:56670377				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					

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Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Borchers,A.H. and Dobie,K.W.
TITLE Antisense modulation of hematopoietic cell protein tyrosine kinase
expression
JOURNAL Patent: US 6828151-A 48 07-DEC-2004;
FEATURES Location/Qualifiers
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Best Local Similarity 83.3%; Pred. No. 2.2e+04;
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Qy 2 ACCGCATAGACTTCTCAG 19
Db 20 AACTCAITGACTTCTCAG 3

RESULT 3
LOCUS AR633611 20 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 12 from patent US 6849399.
ACCESSION AR633611
VERSION AR633611.1 GI:59783856
KEYWORDS 'Unknown.'
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Feder,J.N., Schatzman,R.C. and Teuchihaashi,Z.
TITLE Methods and compositions for diagnosis and treatment of iron
misregulation diseases
JOURNAL Patent: US 6849399-A 12 01-FEB-2005;
FEATURES Bio-Rad Laboratories, Inc.; Hercules, CA
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Qy 1 GACCGCATAGACTTCTCAG 19
Db 2 GACAGCACAGACTTCACCG 20

RESULT 4
LOCUS AR096404/c 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 75 from patent US 6007995.
ACCESSION AR096404
VERSION AR096404.1 GI:10025180
KEYWORDS 'Unknown.'
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowseert,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 75 28-DEC-1999;
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ORIGIN

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Qy 4 CGCATAGACTTCTCAGA 20
Db 18 CGCCAGTCTTCTCAGA 2

RESULT 5
LOCUS BD217452/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION BD217452
VERSION BD217452.1 GI:33027222
KEYWORDS JP 2002519015-A/75.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowseert,L.M.
TITLE Antisense modulation of TNFR1 expression
JOURNAL Patent: JP 2002519015-A 75 02-JUL-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002519015-A/75
PD 02-JUL-2002
PF 17-JUN-1999 JP 2000557265
PR 26-JUN-1998 US 09/106038
PI BRENDA F BAKER, LEX M COWSERT
PC C12N15/09,A61K31/7105,A61K31/711,A61K48/00,A61P29/00,A61P43/00,PC
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PC C12N15/00
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Qy 4 CGCATAGACTTCTCAGA 20
Db 18 CGCCAGTCTTCTCAGA 2

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DEFINITION Sequence 11 from patent US 6849399.
ACCESSION AR633610
VERSION AR633610.1 GI:59783854
KEYWORDS 'Unknown.'
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Feder,J.N., Schatzman,R.C. and Teuchihaashi,Z.
TITLE Methods and compositions for diagnosis and treatment of iron
misregulation diseases
JOURNAL Patent: US 6849399-A 11 01-FEB-2005;
FEATURES Bio-Rad Laboratories, Inc.; Hercules, CA
    Location/Qualifiers

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QY 1 GACCGCATAGACTTCTC 17
Db 2 GACGACACAGCTTCTAC 18

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LOCUS AR031072 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5861504.
ACCESSION AR031072
VERSION AR031072.1 GI:5944286
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AR031072.1 (bases 1 to 20)
Detection of neoplasia by analysis of saliva
Patent: JP 2002505888-A 113 26-FEB-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Artificial Sequence
PN JP 2002505888-A/113
PD 26-FEB-2002
PP 10-MAR-1999 JP 2000535774
PR 10-MAR-1998 US 09/038637
PI DAVID SIDLANSKI
PC C12N15/09, C12Q1/68, C12N15/00
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RESULT 10
AX735344/c
LOCUS AX735344 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 934 from Patent WO03025177.
ACCESSION AX735344
VERSION AX735344.1 GI:30514621
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 03025177-A 934 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTTCTC 17
Db 2 GACGACACAGCTTCTAC 18

RESULT 7
LOCUS AR031072 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5861504.
ACCESSION AR031072
VERSION AR031072.1 GI:5944286
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AR031072.1 (bases 1 to 20)
Detection of neoplasia by analysis of saliva
Patent: JP 2002505888-A 113 26-FEB-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Artificial Sequence
PN JP 2002505888-A/113
PD 26-FEB-2002
PP 10-MAR-1999 JP 2000535774
PR 10-MAR-1998 US 09/038637
PI DAVID SIDLANSKI
PC C12N15/09, C12Q1/68, C12N15/00
CC nucleotide
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Query Match 60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTTCTCAGA 20
Db 1 GACCCACAGCCTATTTCAGA 20

RESULT 8
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LOCUS AR152833 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 113 from patent US 6235470.
ACCESSION AR152833
VERSION AR152833.1 GI:15120365
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
AUTHORS
TITLE
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Patent: US 6235470-A 113 22-MAY-2001;
Detection of neoplasia by analysis of saliva
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Query Match 60.0%; Score 12; DB 2; Length 20;
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Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTTCTCAGA 20
Db 1 GACCCACAGCCTATTTCAGA 20

RESULT 8
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LOCUS AR152833 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 113 from patent US 6235470.
ACCESSION AR152833
VERSION AR152833.1 GI:15120365
KEYWORDS
SOURCE
ORGANISM
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Unclassified.
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TITLE
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Patent: US 6235470-A 113 22-MAY-2001;
Detection of neoplasia by analysis of saliva
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Best Local Similarity 75.0%; Pred. No. 1.1e+05;
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Db      17 CATAAACTCTCTGA 3
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AX759065 Locus      17 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION Sequence 2386 from Patent WO03040369.
ACCESSION AX759065
VERSION   AX759065.1 GI:32253681
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE     Hominidae; Homo.
JOURNAL   Telerman,A., Anson,R. and Tuijinder,M.
          Sequences involved in tumoral suppression, tumoral reversion,
          apoptosis and/or viral resistance phenomena and their use as
          medicines
          Patent: WO 03040369-A 2386 15-MAY-2003;
          Molecular Engines Laboratories (FR)
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RESULT 12
A65727 Locus      18 bp      DNA      linear      PAT 29-MAR-1999
DEFINITION Sequence 8 from Patent WO9735973.
ACCESSION A65727
VERSION   A65727.1 GI:4531346
KEYWORDS  unidentified
SOURCE    unidentified
ORGANISM  unclassified sequences.
REFERENCE 1
AUTHORS   Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and
          Strosberg,A.D.
TITLE     CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF
JOURNAL   Patent: WO 9735973-A 8 02-OCT-1997;
          VETIGEN (FR)
COMMENT   Other publication FR 2746813 19971003.
FEATURES  Location/Qualifiers
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RESULT 13
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LOCUS      AR048183 Sequence 1 from patent US 5821062. 18 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION AR048183
ACCESSION  AR048183
VERSION    AR048183.1 GI:5970526
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Komai,K., Kaneko,H. and Nakatsuka,I.
TITLE      Oligonucleotide for use in checking presence or absence of mutation
          in human-derived cytochrome P450IIC18 gene
          Patent: US 5821062-A 1 13-OCT-1998;
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Best Local Similarity 86.7%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 CATAGACTTCTCAGA 20
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Db      16 CATAGACTTTTGAGA 2

RESULT 14
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LOCUS      E10136 PCR primer to amplify mutated genes encoding human cytochrome
DEFINITION P450IIC18.
ACCESSION  E10136
VERSION    E10136.1 GI:22026764
KEYWORDS   JP 1995285987-A/1.
SOURCE     unidentified
ORGANISM   unclassified sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Komai,K., Kaneko,H. and Nakatsuka,I.
TITLE      OLIGONUCLEOTIDE FOR AMPLIFYING MUTATION TYPE GENE OF HUMAN DERIVED
          CYTOCHROME P450IIC18
          Patent: JP 1995285987-A 1 31-OCT-1995;
          SUMITOMO CHEM CO LTD
JOURNAL    OS None
COMMENT     OC Artificial sequences.
          PN JP 1995285987-A/1
          PD 31-OCT-1995
          PF 29-MAR-1994 JP 1994059386
          PI KOMAI KOICHIRO, KANEKO HIDEO, NAKATSUKA IWAO
          PC C07H21/04,C12Q1/68//C12N15/09;
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Best Local Similarity 86.7%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 15
DD200317
LOCUS DD200317 19 bp RNA linear PAT 19-JAN-2006
DEFINITION RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta
Receptor Gene Expression Using Short Interfering Nucleic Acid
(siNA).
ACCESSION DD200317
VERSION DD200317.1 GI:85651394
KEYWORDS JP 2005517423-A/26.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Beigelman,L. and Mcswiggen,J.
TITLE RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta
Receptor Gene Expression Using Short Interfering Nucleic Acid
(siNA)
JOURNAL Patent: JP 2005517423-A 26 16-JUN-2005;
SiRNA Therapeutics Inc
COMMENT OS Artificial Sequence
PN JP 2005517423-A/26
PD 16-JUN-2005
PF 11-FEB-2003 JP 2003569157
PR 06-JUN-2002 US 60/386782,20-FEB-2002 US 60/358580, PR
15-JAN-2003 US 60/440129,12-NOV-2002 US 60/425559, PR
09-SEP-2002 US 60/409293,11-MAR-2002 US 60/363124, PR
29-AUG-2002 US 60/406784,05-SEP-2002 US 60/408378 PI leonid
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FH Key Location/Qualifiers.
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Best Local Similarity 86.7%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Title: US-09-743-825-10

Perfect score: 20

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 14588

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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4	9.8	49.0	14	13	CZ174508 M1AA-25J1
5	9.8	49.0	14	13	CZ174914 M1AA-21H0
6	9.8	49.0	14	13	CZ175608 M1AA-6H17
7	9.8	49.0	14	13	CZ176205 M1AA-3D24
8	9.8	49.0	14	13	CZ176783 M1AA-2K22
9	9.8	49.0	14	13	CZ177803 M1AA-3D23
10	9.8	49.0	18	14	AJ840659 Arabidops
11	9.8	49.0	19	11	AZ309643 IM0016E23
12	9.8	49.0	20	13	CZ179140 M1AA-5L06
13	9.6	48.0	20	11	AZ660128 IM0538G04
14	9.2	46.0	15	13	CZ172236 M1AA-3K13
15	9.2	46.0	16	13	CZ178031 M1AA-3N19
16	9.2	46.0	17	13	CL681189 PRI0130b
17	9	45.0	18	3	BQ593906 S015504-0
18	9	45.0	19	1	AJ671616 AJ671616
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25	8.8	44.0	13	13	CZ178075	CZ178075 M1AA-6M22
26	8.8	44.0	14	13	CZ172210	CZ172210 M1AA-3K21
27	8.8	44.0	14	13	CZ172211	CZ172211 M1AA-3K21
28	8.8	44.0	14	13	CZ172230	CZ172230 M1AA-3C23
29	8.8	44.0	14	13	CZ173048	CZ173048 M1AA-30I7
30	8.8	44.0	14	13	CZ173186	CZ173186 M1AA-27G2
31	8.8	44.0	14	13	CZ173386	CZ173386 M1AA-22O0
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35	8.8	44.0	14	13	CZ175457	CZ175457 M1AA-8K11
36	8.8	44.0	14	13	CZ175590	CZ175590 M1AA-6N17
37	8.8	44.0	14	13	CZ175976	CZ175976 M1AA-11J0
38	8.8	44.0	14	13	CZ176028	CZ176028 M1AA-3L18
39	8.8	44.0	14	13	CZ176204	CZ176204 M1AA-3L10
40	8.8	44.0	14	13	CZ176662	CZ176662 M1AA-8D05
41	8.8	44.0	14	13	CZ176811	CZ176811 M1AA-15L0
42	8.8	44.0	14	13	CZ177106	CZ177106 M1AA-20H2
43	8.8	44.0	14	13	CZ177302	CZ177302 M1AA-20D1
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45	8.8	44.0	14	13	CZ178072	CZ178072 M1AA-6C18

ALIGNMENTS

RESULT 1
CO792214
LOCUS
DEFINITION
NT014C A10 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5', similar to hypothetical protein, mRNA sequence.
ACCESSION
CO792214
VERSION
CO792214.1
KEYWORDS
EST.
SOURCE
Ambystoma mexicanum (axolotl)
ORGANISM
Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae; Ambystoma.
REFERENCE
1 (bases 1 to 19)
Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K., Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M. An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries
Genome Biol. (2004) In press
Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics, Dresden
Protenhauerstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT014C Row: 10 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1. 19
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Neural Tube, Notochord, Somites"
/cell_type="Includes Neural tube, notochord, somites"
/dev_stage="Stage 18-22"
/clone_lib="St18-22 Neural tube (NT)"
/note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI; Unnormalized cDNA plasmid library prepared by inverted. Size fractionated mRNA was polydT primed and cloned into

NotI-Sall site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 kb.
TAG_LIB=NT"

ORIGIN

Query Match 51.0%; Score 10.2; DB 8; Length 19;
Best Local Similarity 80.0%; Pred. No. 2.1e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGGCATAGACTTCTC 17
||||| |||||

Db 1 CGCAGAGGCTTCAC 15
||||| |||||

RESULT 2

CZ172219

LOCUS

DEFINITION M1AA-3G17c.g1 Meloidogyne incognita BAC end sequence library
(M1AAGSS 001) Meloidogyne incognita genomic, genomic survey
sequence.

ACCESSION

VERSION CZ172219

KEYWORDS

SOURCE GSS.

ORGANISM

Meloidogyne incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE

1 (bases 1 to 14)

AUTHORS

Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.

TITLE

Genome Survey sequences from the parasitic nematode Meloidogyne
incognita

JOURNAL

COMMENT Unpublished (2005)

Contact: Mitreva M

Washington University in St. Louis

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: nematode@watson.wustl.edu

BAC ends sequenced by Washington University Genome Sequencing
Center

Class: BAC ends.

Location/Qualifiers

1. 14

/organism="Meloidogyne incognita"

/mol_type="genomic DNA"

/strain="Race 1"

/db_xref="taxon:6306"

/dev_stage="L2"

/clone_lib="Meloidogyne incognita BAC end sequence library
(M1AAGSS 001)"

/note="Vector: pCGU1; Site 1: HindIII; Site 2: HindIII;
BAC library constructed by Arief Budiman and Nathan Lakey
at Orion Genomics, and David Bird and Charles Opperman at
Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
||||| |||||

Db 2 ATAGAATCTCAG 14
||||| |||||

RESULT 3

CZ174095

LOCUS

DEFINITION M1AA-25J15b.g1 Meloidogyne incognita BAC end sequence library
(M1AAGSS 001) Meloidogyne incognita genomic, genomic survey
sequence.

ACCESSION

VERSION CZ174095

KEYWORDS

SOURCE GSS.

ORGANISM

Meloidogyne incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE

1 (bases 1 to 14)

AUTHORS

Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.

TITLE

Genome Survey sequences from the parasitic nematode Meloidogyne
incognita

JOURNAL

COMMENT Unpublished (2005)

Contact: Mitreva M

Washington University in St. Louis

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: nematode@watson.wustl.edu

BAC ends sequenced by Washington University Genome Sequencing
Center

Class: BAC ends.

Location/Qualifiers

1. 14

/organism="Meloidogyne incognita"

/mol_type="genomic DNA"

/strain="Race 1"

/db_xref="taxon:6306"

/dev_stage="L2"

/clone_lib="Meloidogyne incognita BAC end sequence library
(M1AAGSS 001)"

/note="Vector: pCGU1; Site 1: HindIII; Site 2: HindIII;
BAC library constructed by Arief Budiman and Nathan Lakey
at Orion Genomics, and David Bird and Charles Opperman at
Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
Best Local Similarity 84.6%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
||||| |||||

Db 2 ATAGAATCTCAG 14
||||| |||||

RESULT 4

CZ174508

LOCUS

DEFINITION M1AA-26N17b.g1 Meloidogyne incognita BAC end sequence library
(M1AAGSS 001) Meloidogyne incognita genomic, genomic survey
sequence.

ACCESSION

VERSION CZ174508

KEYWORDS

SOURCE GSS.

ORGANISM

Meloidogyne incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE

1 (bases 1 to 14)

AUTHORS

Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.

TITLE

Genome Survey sequences from the parasitic nematode Meloidogyne
incognita

JOURNAL

COMMENT Unpublished (2005)

Contact: Mitreva M

Washington University in St. Louis

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: nematode@watson.wustl.edu

BAC ends sequenced by Washington University Genome Sequencing Center

FEATURES

source
 Class: BAC ends.
 Location/Qualifiers
 1. .14
 /organism="Meloiodogyne incognita"
 /mol_type="genomic DNA"
 /strain="Race 1"
 /db_xref="taxon:6306"
 /dev_stage="L2"
 /clone_lib="Meloiodogyne incognita BAC end sequence library (MIAAGSS 001)"
 /note="Vector: pCUG1; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAG 19
 |||||
 Db 2 ATAGAATACTCAG 14

RESULT 5

CZ174914
 LOCUS
 DEFINITION
 MIAA-21H08b.g1 Meloiodogyne incognita BAC end sequence library (MIAAGSS 001) Meloiodogyne incognita genomic, genomic survey sequence.

ACCESSION

VERSION
 CZ174914.1 GI:58343207

KEYWORDS

SOURCE

ORGANISM
 Meloiodogyne incognita (southern root-knot nematode)

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

1 (bases 1 to 14)

REFERENCE
 AUTHORS
 Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T., Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.

TITLE
 Genome Survey sequences from the parasitic nematode Meloiodogyne incognita

JOURNAL

COMMENT

Unpublished (2005)
 Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 BAC ends sequenced by Washington University Genome Sequencing Center

FEATURES

source
 Class: BAC ends.
 Location/Qualifiers
 1. .14
 /organism="Meloiodogyne incognita"
 /mol_type="genomic DNA"
 /strain="Race 1"
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 /clone_lib="Meloiodogyne incognita BAC end sequence library (MIAAGSS 001)"
 /note="Vector: pCUG1; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.3e+06;

Matches

11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAG 19
 |||||
 Db 2 ATAGAATACTCAG 14

RESULT 6

CZ175608
 LOCUS
 DEFINITION
 MIAA-6H17c.g1 Meloiodogyne incognita BAC end sequence library (MIAAGSS 001) Meloiodogyne incognita genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Meloiodogyne incognita (southern root-knot nematode)
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2005)
 Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 BAC ends sequenced by Washington University Genome Sequencing Center

Class: BAC ends.

Location/Qualifiers

1. .14

/organism="Meloiodogyne incognita"

/mol_type="genomic DNA"

/strain="Race 1"

/db_xref="taxon:6306"

/dev_stage="L2"

/clone_lib="Meloiodogyne incognita BAC end sequence library (MIAAGSS 001)"

/note="Vector: pCUG1; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAG 19
 |||||
 Db 2 ATAGAATACTCAG 14

RESULT 7

CZ176205
 LOCUS
 DEFINITION
 MIAA-3D24c.g1 Meloiodogyne incognita BAC end sequence library (MIAAGSS 001) Meloiodogyne incognita genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Meloiodogyne incognita (southern root-knot nematode)
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Meloiodogynidae; Meloiodogyninae; Meloiodogyne.

REFERENCE 1 (bases 1 to 14)
 AUTHORS Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T., Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
 TITLE Genome Survey sequences from the parasitic nematode *Meloidogyne incognita*
 JOURNAL Unpublished (2005)
 COMMENT Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 BAC ends sequenced by Washington University Genome Sequencing Center
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..14
 /organism="Meloidogyne incognita"
 /mol_type="genomic DNA"
 /strain="Race 1"
 /db_xref="taxon:6306"
 /dev_stage="L2"
 /clone_lib="Meloidogyne incognita BAC end sequence library (MIAAGSS 001)"
 /note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 ATAGACTTCTCAG 19
 ||||| |||||
 Db 2 ATAGAATACTCAG 14

RESULT 8
 C2176783
 LOCUS MIAA-22K24b.g1 Meloidogyne incognita BAC end sequence library
 DEFINITION (MIAAGSS 001) Meloidogyne incognita genomic, genomic survey sequence.
 VERSION C2176783
 KEYWORDS GSS.
 SOURCE Meloidogyne incognita (southern root-knot nematode)
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 14)
 AUTHORS Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T., Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
 TITLE Genome Survey sequences from the parasitic nematode *Meloidogyne incognita*
 JOURNAL Unpublished (2005)
 COMMENT Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 BAC ends sequenced by Washington University Genome Sequencing Center
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..14
 /organism="Meloidogyne incognita"
 /mol_type="genomic DNA"

/strain="Race 1"
 /db_xref="taxon:6306"
 /dev_stage="L2"
 /clone_lib="Meloidogyne incognita BAC end sequence library (MIAAGSS 001)"
 /note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 ATAGACTTCTCAG 19
 ||||| |||||
 Db 2 ATAGAATACTCAG 14

RESULT 9

C2178035
 LOCUS MIAA-3D23c.g1 Meloidogyne incognita BAC end sequence library
 DEFINITION (MIAAGSS 001) Meloidogyne incognita genomic, genomic survey sequence.
 ACCESSION C2178035
 VERSION C2178035.1 GI:58346328
 KEYWORDS GSS.
 SOURCE Meloidogyne incognita (southern root-knot nematode)
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 14)
 AUTHORS Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T., Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
 TITLE Genome Survey sequences from the parasitic nematode *Meloidogyne incognita*
 JOURNAL Unpublished (2005)
 COMMENT Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 BAC ends sequenced by Washington University Genome Sequencing Center
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..14
 /organism="Meloidogyne incognita"
 /mol_type="genomic DNA"
 /strain="Race 1"
 /db_xref="taxon:6306"
 /dev_stage="L2"
 /clone_lib="Meloidogyne incognita BAC end sequence library (MIAAGSS 001)"
 /note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 49.0%; Score 9.8; DB 13; Length 14;
 Best Local Similarity 84.6%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 ATAGACTTCTCAG 19
 ||||| |||||
 Db 2 ATAGAATACTCAG 14

RESULT 10	AJ840659	Arabidopsis thaliana T-DNA flanking sequence, right border, clone 604E10, genomic survey sequence.	18 bp	DNA	linear	GSS 08-FEB-2006
LOCUS	AJ840659					
DEFINITION	AJ840659	Arabidopsis thaliana T-DNA flanking sequence.				
ACCESSION	AJ840659					
VERSION	AJ840659.1	GI:52544865				
KEYWORDS		GSS; right border; T-DNA flanking sequence.				
SOURCE		Arabidopsis thaliana (thale cress)				
ORGANISM		Arabidopsis thaliana				
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.				
REFERENCE	1	Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.				
AUTHORS		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites				
TITLE		EMBO Rep. 3 (12), 1152-1157 (2002)				
JOURNAL		12446565				
PUBMED						
REFERENCE	2	(bases 1 to 18)				
AUTHORS		Balzerque, S.				
TITLE		Direct Submission				
JOURNAL		Submitted (21-SEP-2004) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE				
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).				
FEATURES		Location/Qualifiers				
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		/mol_type="genomic DNA"				
		/cultivar="Wassiliewskija"				
		/db_xref="taxon:3702"				
		/clone="604E10"				
		/clone_lib="Arabidopsis thaliana T-DNA insertion lines"				
		/ecotype="Wassiliewskija"				
misc_feature	1..18	/note="T-DNA flanking sequence right border"				
ORIGIN						
Query Match	49.0%;	Score 9.8; DB 14; Length 18;				
Best Local Similarity	84.6%;	Pred. No. 3.4e+06;				
Matches	11; Conservative	0; Mismatches 2; Indels 0; Gaps 0;				
Qy	8	TAGACTTCTCAGA 20				
Db	2	TAGATTGTTCAGA 14				
RESULT 11	AZ309643	Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0016223 F, genomic survey sequence.	19 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	AZ309643					
DEFINITION	AZ309643	Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0016223 F, genomic survey sequence.				
ACCESSION	AZ309643					
VERSION	AZ309643.1	GI:10350661				
KEYWORDS		GSS.				
SOURCE		Mus musculus (house mouse)				
ORGANISM		Mus musculus				
		Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
REFERENCE	1	MIAA-SL06b.g1 Meloidogyne incognita BAC end sequence library (MIAAGSS 001) Meloidogyne incognita genomic, genomic survey sequence.	20 bp	DNA	linear	GSS 31-JAN-2005
AUTHORS		CZ179140				
TITLE		LOCUS				
JOURNAL		DEFINITION				
COMMENT		Accession				
		Version				
		Keywords				
		Source				
		Organism				
		Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;				

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REFERENCE
AUTHORS      Tylenchoidae; Meloidegynidae; Meloidegyninae; Meloidegynae.
1 (bases 1 to 20)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidegynae
incognita
JOURNAL      Unpublished (2005)
COMMENT      Contact: Mitreva M
Washington University in St. Louis
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
Class: BAC ends.
Location/Qualifiers
1..20
/organism="Meloidegynae incognita"
/mol_type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
/dev_stage="L2"
/clone_lib="Meloidegynae incognita BAC end sequence library
(MIAAGSS 001)"
/note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII;
BAC library constructed by Arief Budiman and Nathan Lakey
at Orion Genomics, and David Bird and Charles Opperman at
Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN
Query Match      49.0%; Score 9.8; DB 13; Length 20;
Best Local Similarity 84.6%; Pred. No. 3.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAG 19
||||| |
DB 2 ATAGAATCTCAG 14

RESULT 13
AZ660128/c
LOCUS
DEFINITION      20 bp DNA linear GSS 14-DEC-2000
1M0538G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0538G04 F, genomic survey sequence.
ACCESSION      AZ660128
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0538 row: G column: 04
Seq primer: CGTTGAAACGACGCCAGT

Tylenchoidae; Meloidegynidae; Meloidegyninae; Meloidegynae.
1 (bases 1 to 20)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidegynae
incognita
JOURNAL      Unpublished (2005)
COMMENT      Contact: Mitreva M
Washington University in St. Louis
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
Class: BAC ends.
Location/Qualifiers
1..20
/organism="Meloidegynae incognita"
/mol_type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
/dev_stage="L2"
/clone_lib="Meloidegynae incognita BAC end sequence library
(MIAAGSS 001)"
/note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII;
BAC library constructed by Arief Budiman and Nathan Lakey
at Orion Genomics, and David Bird and Charles Opperman at
Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN
Query Match      49.0%; Score 9.8; DB 13; Length 20;
Best Local Similarity 84.6%; Pred. No. 3.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAG 19
||||| |
DB 2 ATAGAATCTCAG 14

RESULT 13
AZ660128/c
LOCUS
DEFINITION      20 bp DNA linear GSS 14-DEC-2000
1M0538G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0538G04 F, genomic survey sequence.
ACCESSION      AZ660128
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0538 row: G column: 04
Seq primer: CGTTGAAACGACGCCAGT

Tylenchoidae; Meloidegynidae; Meloidegyninae; Meloidegynae.
1 (bases 1 to 20)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidegynae
incognita
JOURNAL      Unpublished (2005)
COMMENT      Contact: Mitreva M
Washington University in St. Louis
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
Class: BAC ends.
Location/Qualifiers
1..15
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0538G04"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      48.0%; Score 9.6; DB 11; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.4e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GCATAGACTTCTCAGA 20
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DB 20 GCATAGATATATCAT 5

RESULT 14
CZ172236
LOCUS
DEFINITION      15 bp DNA linear GSS 31-JAN-2005
M1AA-3K13c.g1 Meloidegynae incognita BAC end sequence library
(M1AAGSS 001) Meloidegynae incognita genomic, genomic survey
sequence.
ACCESSION      CZ172236
VERSION
KEYWORDS
SOURCE
ORGANISM
Meloidegynae incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidae; Meloidegynidae; Meloidegyninae; Meloidegynae.
1 (bases 1 to 15)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidegynae
incognita
Unpublished (2005)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
Class: BAC ends.
Location/Qualifiers
1..15

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/organism="Meloiodogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
/dev_stage="L2"
/clone_lib="Meloiodogyne incognita BAC end sequence library (MIAAGSS 001)"
/note="Vector: pCUG1; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 46.0%; Score 9.2; DB 13; Length 15;
Best Local Similarity 78.6%; Pred. No. 7e+06; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAGA 20
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Db 2 ATAGAATACTCAAA 15

RESULT 15
C2178031
LOCUS
DEFINITION
MIAA-3N19c.g1 Meloiodogyne incognita BAC end sequence library (MIAAGSS 001) Meloiodogyne incognita genomic, genomic survey sequence.
16 bp DNA linear GSS 31-JAN-2005
ACCESSION
C2178031
VERSION
C2178031.1 GI:58346324
KEYWORDS
GSS.
SOURCE
Meloiodogyne incognita (southern root-knot nematode)
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Meloiodogynidae; Meloiodogyninae; Meloiodogyne.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T., Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
TITLE
Genome Survey sequences from the parasitic nematode Meloiodogyne incognita
JOURNAL
Unpublished (2005)
COMMENT
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing Center
Class: BAC ends.

FEATURES
source
1..16
Location/Qualifiers
/organism="Meloiodogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
/dev_stage="L2"
/clone_lib="Meloiodogyne incognita BAC end sequence library (MIAAGSS 001)"
/note="Vector: pCUG1; Site 1: HindIII; Site 2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."

ORIGIN

Query Match 46.0%; Score 9.2; DB 13; Length 16;
Best Local Similarity 78.6%; Pred. No. 7e+06; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCAGA 20
|||||
Db 2 ATAGAATACTCAAA 15

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Result No.	Query			ID	Description
	Score	Match	Length		
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2	13.2	66.0	20	3	US-10-007-010-48
3	12.6	63.0	20	3	US-08-920-559-12
4	12.2	61.0	18	3	US-09-106-038A-75
5	12.2	61.0	20	3	US-08-920-559-11
6	12	60.0	20	2	US-07-922-723A-60
7	12	60.0	20	2	US-07-799-828C-60
8	12	60.0	20	2	US-07-952-277A-60
9	12	60.0	20	3	US-09-038-637-113
10	11.8	59.0	18	2	US-08-716-459-1
11	11.8	59.0	20	2	US-08-819-912-8
12	11.6	58.0	20	3	US-09-731-457B-14
13	11.4	57.0	15	2	US-08-291-932A-289
14	11.4	57.0	17	3	US-08-434-511-4
15	11.4	57.0	17	3	US-08-229-150-4
16	11.4	57.0	17	10	5403629-5
17	11.4	57.0	19	3	US-09-696-791-1238
18	11.4	57.0	19	3	US-09-696-791-1239
19	11.4	57.0	20	3	US-08-974-180-35
20	11.4	57.0	20	3	US-10-148-806-20
21	11.4	57.0	20	3	US-10-148-806-21
22	11.2	56.0	18	3	US-09-422-978-4697
23	11.2	56.0	20	2	US-07-977-284A-113
					Sequence 2812, Ap Sequence 48, Appl Sequence 12, Appl Sequence 75, Appl Sequence 11, Appl Sequence 60, Appl Sequence 60, Appl Sequence 113, App Sequence 1, Appl Sequence 8, Appl Sequence 14, Appl Sequence 289, App Sequence 4, Appl Sequence 4, Appl Patent No. 5401629 Sequence 1238, Ap Sequence 1239, Ap Sequence 35, Appl Sequence 20, Appl Sequence 21, Appl Sequence 4697, Ap Sequence 113, App

US-10-007-010-48

Query Match 66.0%; Score 13.2; DB 3; Length 20;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACCGCATAGACTTCTCAG 19
 Db 20 AACTCATTGACTTCTCAG 3

RESULT 3

US-08-920-559-12
 ; Sequence 12, Application US/08920559
 ; Patent No. 6849399
 ; GENERAL INFORMATION:
 ; APPLICANT: Feder, John N.
 ; APPLICANT: Schatzman, Randall C.
 ; APPLICANT: Tsuchihashi, Zenta
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS: 13
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/920,559
 ; FILING DATE: 27-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/652,265
 ; FILING DATE: 23-MAY-1996
 ; APPLICATION NUMBER: US 08/834,497
 ; FILING DATE: 04-APR-1997
 ; APPLICATION NUMBER: US 08/866,211
 ; FILING DATE: 13-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Poissant, Brian M
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 8907-0062-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-920-559-12

Query Match 63.0%; Score 12.6; DB 3; Length 20;
 Best Local Similarity 78.9%; Pred. No. 2.9e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCAG 19
 Db 2 GACAGCACAGACTTCACCG 20

RESULT 4

US-09-106-038A-75/c

; Sequence 75, Application US/09106038A
 ; Patent No. 6007995
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenda F. Baker and Lex M. Cowseert
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
 ; NUMBER OF SEQUENCES: 91
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Isis Pharmaceuticals, Inc.
 ; STREET: 2292 Paraday Avenue
 ; CITY: Carlsbad
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92008
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows NT
 ; SOFTWARE: Microsoft Word 97
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/106,038A
 ; FILING DATE: June 26, 1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Laurel Spear Bernstein
 ; REGISTRATION NUMBER: 37,280
 ; REFERENCE/DOCKET NUMBER: RTS-0004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (760) 931-9200
 ; TELEFAX: (760) 603-3820
 ; INFORMATION FOR SEQ ID NO: 75:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-106-038A-75

Query Match 61.0%; Score 12.2; DB 3; Length 18;
 Best Local Similarity 82.4%; Pred. No. 4.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGCATAGACTTCTCAGA 20
 Db 18 CGCCAGTCTTCTCAGA 2

RESULT 5

US-08-920-559-11
 ; Sequence 11, Application US/08920559
 ; Patent No. 6849399
 ; GENERAL INFORMATION:
 ; APPLICANT: Feder, John N.
 ; APPLICANT: Schatzman, Randall C.
 ; APPLICANT: Tsuchihashi, Zenta
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/920,559

Query Match 61.0%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGCGATAGACTTCTC 17
DB 2 GACGCGATAGACTTCTAC 18

RESULT 6
US-07-922-723A-60
; Sequence 60, Application US/07922723A
; Patent No. 5369004
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/922,723A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34506
; REFERENCE/DOCKET NUMBER: 717081B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-920-559-11
Query Match 61.0%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGCGATAGACTTCTC 17
DB 2 GACGCGATAGACTTCTAC 18

RESULT 6
US-07-922-723A-60
; Sequence 60, Application US/07922723A
; Patent No. 5369004
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/922,723A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34506
; REFERENCE/DOCKET NUMBER: 717081B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-07-922-723A-60
Query Match 60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACGCGATAGACTTCTCAGA 20
DB 1 GACCCCGACAGCCTATTTCAGA 20

RESULT 7
US-07-799-828C-60
; Sequence 60, Application US/07799828C
; Patent No. 5378602
; GENERAL INFORMATION:
; APPLICANT: Drs. Carl R. Merrill and
; APPLICANT: Michael H. Polymeropoulos
; TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: MICROSATELLITE REPEAT
; TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/799,828C
; FILING DATE: 19911127
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: D.J. Mills
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 717081A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-07-799-828C-60
Query Match 60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACGCGATAGACTTCTCAGA 20
DB 1 GACCCCGACAGCCTATTTCAGA 20

RESULT 8
US-07-952-277A-60
; Sequence 60, Application US/07952277A
; Patent No. 5861504
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:

US-07-952-277A-60
Query Match 60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACGCGATAGACTTCTCAGA 20
DB 1 GACCCCGACAGCCTATTTCAGA 20

RESULT 8
US-07-952-277A-60
; Sequence 60, Application US/07952277A
; Patent No. 5861504
; GENERAL INFORMATION:
; APPLICANT: Drs. Michael H. Polymeropoulos
; APPLICANT: and Carl R. Merrill
; TITLE OF INVENTION: ELEVEN HIGHLY INFORMATIVE
; TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Lowe, Price, LeBlanc & Becker
;; STREET: Suite 300, 99 Canal Center Plaza
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22314
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: DOS Text File
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/952,277A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: D.J. Mills
;; REGISTRATION NUMBER: 34506
;; REFERENCE/DOCKET NUMBER: 717081C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703 684 1111
;; INFORMATION FOR SEQ ID NO: 60:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-952-277A-60

Query Match 60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACGCGCATAGACTTCTCAGA 20
|||||
Db 1 GACCCACAGCCTATTTCAGA 20

RESULT 9
US-09-038-637-113
; Sequence 113, Application US/09038637
; Patent No. 6235470
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
; NUMBER OF SEQUENCES: 195
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,637
; FILING DATE: 10-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/579,233
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/146001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070

;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
US-09-038-637-113

Query Match 60.0%; Score 12; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACGCGCATAGACTTCTCAGA 20
|||||
Db 1 GACCCACAGCCTATTTCAGA 20

RESULT 10
US-08-716-459-1/c
; Sequence 1, Application US/08716459
; Patent No. 5821062
; GENERAL INFORMATION:
; APPLICANT: KOMAI, Koichiro
; APPLICANT: KANEKO, Hideo
; APPLICANT: NAKATSUKA, Iwao
; TITLE OF INVENTION: OLIGONUCLEOTIDE FOR USE IN CHECKING
; TITLE OF INVENTION: PRESENCE OR ABSENCE OF MUTATION IN
; TITLE OF INVENTION: HUMAN-DERIVED CYTOCHROME P45011C18 GENE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: IBM DOS Version 5.00
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,459
; FILING DATE: 27 SEPTEMBER 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-059385/1994
; APPLICATION NUMBER: JP-059386/1994
; FILING DATE: 29-03-1994
; FILING DATE: 29-03-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-4081PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid synthetic DNA
US-08-716-459-1

Query Match 59.0%; Score 11.8; DB 2; Length 18;
Best Local Similarity 86.7%; Pred. No. 7.6e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CATAGACTTCTCAGA 20
 Db 16 CATAGACTTTTGAGA 2

RESULT 11

US-08-819-912-8
 ; Sequence 8, Application US/08819912
 ; Patent No. 5795722
 ; GENERAL INFORMATION:
 ; APPLICANT: Lacroix, Jean-Michel
 ; APPLICANT: Dunn, James M.
 ; TITLE OF INVENTION: METHOD AND KIT FOR QUANTITATION AND
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCING OF NUCLEIC ACID ANALYTES IN A SAMPLE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Oppedahl & Larson
 ; STREET: 1992 Commerce Street Suite 309
 ; CITY: Yorktown
 ; STATE: NY
 ; COUNTRY: US
 ; ZIP: 10598

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/819,912
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Larson, Marina T.
 ; REGISTRATION NUMBER: 32,038
 ; REFERENCE/DOCKET NUMBER: VGEN.P-039US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 245-3252
 ; TELEFAX: (914) 962-4330
 ; TELEX:

INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: yes
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Chlamydia trachomatis
 ; FEATURE:
 ; OTHER INFORMATION: amplification primer CT1431P for cryptic
 ; OTHER INFORMATION: plasmid

US-08-819-912-8

Query Match 59.0%; Score 11.8; DB 2; Length 20;
 Best Local Similarity 86.7%; Pred. No. 7.7e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCATAGACTTCTCAG 19
 Db 3 GCATAAAGCTTCTGAG 17

RESULT 12

US-09-731-457B-14
 ; Sequence 14, Application US/09731457B
 ; Patent No. 6855700
 ; GENERAL INFORMATION:

; APPLICANT: Ian Popoff
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P
 ; TITLE OF INVENTION: EXPRESSION
 ; FILE REFERENCE: RTS-0182
 ; CURRENT APPLICATION NUMBER: US/09/731,457B
 ; CURRENT FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 14
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 ; US-09-731-457B-14

Query Match 58.0%; Score 11.6; DB 3; Length 20;
 Best Local Similarity 77.8%; Pred. No. 9.9e+03;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTTCTCA 18
 Db 2 GACCACATAGATCTCTAA 19

RESULT 13

US-08-291-932A-289
 ; Sequence 289, Application US/08291932A
 ; Patent No. 5658780
 ; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Draper, Kenneth G.
 ; APPLICANT: McSwiggen, James
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; TITLE OF INVENTION: DISEASES OR CONDITIONS
 ; TITLE OF INVENTION: RELATED TO LEVELS OF
 ; TITLE OF INVENTION: NF-KB
 ; NUMBER OF SEQUENCES: 830
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/291,932A
 ; FILING DATE: August 15, 1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below:
 ; APPLICATION NUMBER: 08/245,466
 ; FILING DATE: May 18, 1994
 ; APPLICATION NUMBER: 07/987,132
 ; FILING DATE: December 7, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 208/157
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 289:
 ; SEQUENCE CHARACTERISTICS:

Two

;
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-289

Query Match 57.0%; Score 11.4; DB 2; Length 15;
Best Local Similarity 61.5%; Pred. No. 1.2e+04;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
|: |||: |||:
Db 1 AUGGACUUCUAG 13

RESULT 14
US-08-434-511-4/c
; Sequence 4, Application US/08434511
; Patent No. 6057114
; GENERAL INFORMATION:
; APPLICANT: Akong, Anthony
; APPLICANT: Harpold, Michael
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Brust, Paul
; TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY
; TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,511
; FILING DATE: 04-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,985
; FILING DATE: 20-JUN-1994
; APPLICATION NUMBER: PCT/US92/11090
; FILING DATE: 18-DEC-1992
; APPLICATION NUMBER: 07/812,254
; FILING DATE: 20-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9738
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-434-511-4

Query Match 57.0%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. NO. 1.2e+04;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 ATAGACTTCTCAG 19
|: |||: |||:
Db 13 ATAGAATTCTCAG 1

RESULT 15
US-08-229-150-4/c
; Sequence 4, Application US/08229150
; Patent No. 6127133
; GENERAL INFORMATION:
; APPLICANT: Akong, Michael A.
; APPLICANT: Harpold, Michael M.
; APPLICANT: Velicelebi, G.
; APPLICANT: Brust, Paul
; TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY METHOD FOR DETECTING CELL
; TITLE OF INVENTION: PROTEIN FUNCTION USING SAME
; FILE REFERENCE: 24735-51505B
; CURRENT APPLICATION NUMBER: US/08/229,150
; CURRENT FILING DATE: 1994-04-18
; EARLIER APPLICATION NUMBER: 07/812,254
; EARLIER FILING DATE: 1991-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for screening of products having
; OTHER INFORMATION: EcoRI site adjacent to initiation codon of human
; OTHER INFORMATION: HMI coding region
US-08-229-150-4

Query Match 57.0%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. NO. 1.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
|: |||: |||:
Db 13 ATAGAATTCTCAG 1

Search completed: June 9, 2006, 01:58:07
Job time : 100 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2006, 01:56:41 ; Search time 839 Seconds
(without alignments)
292.911 Million cell updates/sec

Title: US-09-743-825-10

Perfect score: 20

Sequence: 1 gaccgcagatcttcgacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 9412572

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	14	70.0	19 14	US-11-083-784-577386 Sequence 577386,
2	14	70.0	19 15	US-11-101-244-577386 Sequence 577386,
3	13.8	69.0	19 14	US-11-083-784-818386 Sequence 818386,
4	13.8	69.0	19 14	US-11-083-784-1312885 Sequence 1312885,
5	13.8	69.0	19 15	US-11-101-244-818386 Sequence 818386,
6	13.8	69.0	19 15	US-11-101-244-1312885 Sequence 1312885,
7	13.8	69.0	20 7	US-10-289-762-2812 Sequence 2812, Ap
8	13.4	67.0	19 14	US-11-083-784-189920 Sequence 189920,
9	13.4	67.0	19 14	US-11-083-784-189920 Sequence 189920,
10	13.4	67.0	19 14	US-11-083-784-511937 Sequence 511937,
11	13.4	67.0	19 14	US-11-083-784-1082194 Sequence 1082194,
12	13.4	67.0	19 15	US-11-101-244-189920 Sequence 189920,
13	13.4	67.0	19 15	US-11-101-244-189920 Sequence 189920,
14	13.4	67.0	19 15	US-11-101-244-511937 Sequence 511937,
15	13.4	67.0	19 15	US-11-101-244-1082194 Sequence 1082194,
16	13.2	66.0	19 14	US-11-083-784-1065181 Sequence 1065181,
17	13.2	66.0	19 14	US-11-083-784-1500214 Sequence 1500214,

18	13.2	66.0	19 15	US-11-101-244-1065181 Sequence 1065181,
19	13.2	66.0	19 15	US-11-101-244-1500214 Sequence 1500214,
c 20	13.2	66.0	20 7	US-10-007-010-48 Sequence 48, Appl
c 21	13.2	66.0	20 12	US-10-497-299A-48 Sequence 66572, A
22	13	65.0	19 14	US-11-083-784-66572 Sequence 66572, A
23	13	65.0	19 14	US-11-083-784-66629 Sequence 66629, A
24	13	65.0	19 14	US-11-083-784-66672 Sequence 66672, A
25	13	65.0	19 14	US-11-083-784-66728 Sequence 66728, A
26	13	65.0	19 15	US-11-101-244-66572 Sequence 66572, A
27	13	65.0	19 15	US-11-101-244-66629 Sequence 66629, A
28	13	65.0	19 15	US-11-101-244-66672 Sequence 66672, A
29	13	65.0	19 15	US-11-101-244-66728 Sequence 66728, A
30	12.8	64.0	18 11	US-10-310-914A-1316661 Sequence 1316661,
c 31	12.8	64.0	19 14	US-11-083-784-36613 Sequence 36613, A
32	12.8	64.0	19 14	US-11-083-784-792624 Sequence 792624,
c 33	12.8	64.0	19 14	US-11-083-784-928451 Sequence 928451,
c 34	12.8	64.0	19 14	US-11-083-784-928550 Sequence 928550,
35	12.8	64.0	19 14	US-11-083-784-1267201 Sequence 1267201,
36	12.8	64.0	19 14	US-11-083-784-1312824 Sequence 1312824,
37	12.8	64.0	19 14	US-11-083-784-1324218 Sequence 1324218,
38	12.8	64.0	19 14	US-11-083-784-1324219 Sequence 1324219,
c 39	12.8	64.0	19 14	US-11-083-784-1498706 Sequence 1498706,
40	12.8	64.0	19 14	US-11-083-784-1500216 Sequence 1500216,
c 41	12.8	64.0	19 15	US-11-101-244-36613 Sequence 36613, A
42	12.8	64.0	19 15	US-11-101-244-792624 Sequence 792624,
c 43	12.8	64.0	19 15	US-11-101-244-928451 Sequence 928451,
c 44	12.8	64.0	19 15	US-11-101-244-928550 Sequence 928550,
45	12.8	64.0	19 15	US-11-101-244-1267201 Sequence 1267201,

ALIGNMENTS

RESULT 1

US-11-083-784-577386
; Sequence 577386, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 577386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-577386

Query Match 70.0%; Score 14; DB 14; Length 19;
Best Local Similarity 78.6%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACGCGTAGACTT 14

Db 6 GACGCGTAGACTT 19

RESULT 2

US-11-101-244-577386

; Sequence 577386, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 577386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-577386

Query Match 70.0%; Score 14; DB 15; Length 19;
Best Local Similarity 78.6%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTT 14
DB 6 GACCGCAUAGACUU 19

RESULT 3

US-11-083-784-818386/C
; Sequence 818386, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 818386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-818386

Query Match 69.0%; Score 13.8; DB 14; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGCATAGACTTCTCA 18
DB 19 ACATCATAGACTTCTCA 3

RESULT 4

US-11-083-784-1312885
; Sequence 1312885, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1312885
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1312885

Query Match 69.0%; Score 13.8; DB 14; Length 19;
Best Local Similarity 70.6%; Pred. No. 4.6e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCATAGACTTCTCAGA 20
DB 1 CGCAAGCCUUCUCAGA 17

RESULT 5

US-11-101-244-818386/C
; Sequence 818386, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 818386
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-818386

Query Match 69.0%; Score 13.8; DB 15; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCGCATAGACTTCTCA 18
DB 19 ACATCATAGACTTCTCA 3

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RESULT 6
US-11-101-244-1312885
; Sequence 1312885, Application US/11101244
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1312885
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1312885

Query Match 69.0%; Score 13.8; DB 15; Length 19;
Best Local Similarity 70.6%; Pred. No. 4.6e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCATAGACTTCTCAGA 20
Db 1 GCCTAAGCCUUCUCAGA 17

RESULT 7
US-10-289-762-2812
; Sequence 2812, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2812
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2812

Query Match 69.0%; Score 13.8; DB 7; Length 20;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTC 17
Db 3 GACCGCATAACTTATC 19

RESULT 8
US-11-083-784-189820
; Sequence 189820, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 189820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-189820

Query Match 67.0%; Score 13.4; DB 14; Length 19;
Best Local Similarity 73.3%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTCAG 19
Db 1 GCAUAGAGCUCUCAG 15

RESULT 9
US-11-083-784-189920
; Sequence 189920, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 189920
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-189920

Query Match 67.0%; Score 13.4; DB 14; Length 19;
Best Local Similarity 73.3%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTCAG 19
Db 1 GCAUAGAGCUCUCAG 15

RESULT 10
US-11-083-784-511937/c
; Sequence 511937, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 511937
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-511937

Query Match 67.0%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCAGA 20
|||:|||||:
Db 15 CATAGACTTCTCAAA 1

RESULT 11
US-11-083-784-1082194
; Sequence 1082194, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1082194
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1082194

Query Match 67.0%; Score 13.4; DB 14; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCAGA 20
||:|||||:
Db 1 CAUCGACUUCUCAGA 15

RESULT 12
US-11-101-244-189820
; Sequence 189820, Application US/11101244

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 189820
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-189820

Query Match 67.0%; Score 13.4; DB 15; Length 19;
Best Local Similarity 73.3%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTCAG 19
|||:|||||:
Db 1 GCAUAGACGUCUCAG 15

RESULT 13
US-11-101-244-189920
; Sequence 189920, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 189920
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-189920

Query Match 67.0%; Score 13.4; DB 15; Length 19;
Best Local Similarity 73.3%; Pred. No. 7.6e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTCAG 19
|||:|||||:
Db 1 GCAUAGACGUCUCAG 15

RESULT 14
US-11-101-244-511937/c
; Sequence 511937, Application US/11101244
; Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
PRIOR FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 511937
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-511937

Query Match 67.0%; Score 13.4; DB 15; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 CATAGACTTCTCAGA 20
Db 15 CATAGACTTCTCAGA 1

RESULT 15
US-11-101-244-1082194
Sequence 1082194, Application US/11/101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
PRIOR FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1082194
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1082194

Query Match 67.0%; Score 13.4; DB 15; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 6 CATAGACTTCTCAGA 20
Db 1 CAUCGACUUCUCAGA 15

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Job time : 840 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-743-825-10

Perfect score: 20

Sequence: 1 gacgcctagactcttcaga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 253354 seqs, 63461778 residues

Total number of hits satisfying chosen parameters: 16344

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	20	7	US-11-189-279-45
C 2	10	50.0	19	6	US-10-514-776-214
C 3	10	50.0	19	7	US-11-251-465-365
C 4	10	50.0	20	7	US-11-264-558-38
C 5	9.8	49.0	20	6	US-10-511-937-993
C 6	9.6	48.0	18	7	US-11-293-697-5435
C 7	9.6	48.0	20	7	US-11-247-332-2
C 8	9.2	46.0	19	7	US-11-251-465-371
C 9	9.2	46.0	20	6	US-10-511-937-704
C 10	9.2	46.0	20	6	US-10-469-938A-158
C 11	9	45.0	18	6	US-11-251-465-201
C 12	9	45.0	19	7	US-11-264-737-358
C 13	8.8	44.0	18	7	US-11-233-507-18
C 14	8.8	44.0	19	6	US-10-521-008-6
C 15	8.8	44.0	19	6	US-10-524-399-14
C 16	8.8	44.0	19	7	US-11-264-784-256
C 17	8.8	44.0	19	7	US-11-264-737-358
C 18	8.8	44.0	19	7	US-11-265-761-268
C 19	8.8	44.0	20	6	US-10-474-853-41
C 20	8.8	44.0	20	6	US-10-511-832-21
C 21	8.8	44.0	20	6	US-10-620-289-16
C 22	8.8	44.0	20	6	US-10-857-260-19
C 23	8.8	44.0	20	7	US-11-251-465-875
C 24	8.8	44.0	20	7	US-11-324-230-4
C 25	8.6	43.0	15	7	US-11-110-361A-84

26	8.6	43.0	18	7	US-11-293-697-5287	Sequence 5287, Ap
27	8.6	43.0	19	6	US-10-511-937-2016	Sequence 2016, Ap
C 28	8.6	43.0	20	6	US-10-514-776-28	Sequence 28, Appl
C 29	8.6	43.0	20	6	US-10-514-776-215	Sequence 215, Appl
C 30	8.6	43.0	20	6	US-10-511-832-76	Sequence 76, Appl
C 31	8.6	43.0	20	7	US-11-123-692-10	Sequence 10, Appl
C 32	8.6	43.0	20	7	US-11-255-980-10	Sequence 10, Appl
C 33	8.4	42.0	11	7	US-11-158-209-32	Sequence 32, Appl
C 34	8.4	42.0	17	6	US-10-499-286-25	Sequence 25, Appl
C 35	8.4	42.0	18	7	US-11-293-697-5317	Sequence 5317, Ap
C 36	8.4	42.0	19	6	US-10-514-776-442	Sequence 442, App
C 37	8.4	42.0	19	7	US-11-251-465-321	Sequence 321, App
C 38	8.4	42.0	19	7	US-11-251-465-847	Sequence 847, App
C 39	8.4	42.0	19	7	US-11-293-697-5255	Sequence 5255, Ap
C 40	8.4	42.0	20	6	US-10-511-937-726	Sequence 726, App
C 41	8.4	42.0	20	6	US-10-514-776-167	Sequence 167, App
C 42	8.4	42.0	20	6	US-10-514-776-177	Sequence 177, App
C 43	8.4	42.0	20	6	US-10-514-776-199	Sequence 199, App
C 44	8.4	42.0	20	6	US-10-525-817-115	Sequence 115, App
C 45	8.4	42.0	20	6	US-10-525-817-116	Sequence 116, App

ALIGNMENTS

RESULT 1
US-11-189-279-45/c
; Sequence 45, Application US/11189279
; Publication No. US20060115829A1
; GENERAL INFORMATION:
; APPLICANT: MAO, LI
; APPLICANT: WANG, JIE
; APPLICANT: LUO, WANG
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: UTXC:875US
; CURRENT APPLICATION NUMBER: US/11/189,279
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: 60/598,554
; PRIOR FILING DATE: 2004-08-03
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-189-279-45

Query Match 60.0%; Score 12; DB 7; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACCGCATGACTTCTCAGA 20
Db 20 GACCTCAGACACACAGA 1

RESULT 2
US-10-514-776-214/c
; Sequence 214, Application US/10514776
; Publication No. US20060094008A1
; GENERAL INFORMATION:
; APPLICANT: Symex Corporation
; TITLE OF INVENTION: CK primer
; FILE REFERENCE: GP03-1006PCT
; CURRENT APPLICATION NUMBER: US/10/514,776
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: JP P2002-145689
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: JP P2002-175271
; PRIOR FILING DATE: 2002-06-17

; PRIOR APPLICATION NUMBER: JP P2002-199759
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed DNA based on CK18
US-10-514-776-214

Query Match 50.0%; Score 10; DB 6; Length 19;
Best Local Similarity 72.2%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ACCGCATAGACTTCTCAG 19
||| ||| ||| ||| ||| |||
Db 19 ACCACACAGTCGTCTGAG 2

RESULT 3
US-11-251-465-365/c
; Sequence 365, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 365
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-365

Query Match 50.0%; Score 10; DB 7; Length 19;
Best Local Similarity 72.2%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACGCATAGACTTCTCA 18
||| ||| ||| ||| ||| |||
Db 18 GAGCACAAGACTCCACA 1

RESULT 4
US-11-264-558-38/c
; Sequence 38, Application US/11264558
; Publication No. US20060088913A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; APPLICANT: Harkin, Louise A
; APPLICANT: Dibbens, Leanne M
; TITLE OF INVENTION: MUTATION ASSOCIATED WITH EPILEPSY
; FILE REFERENCE: 1386/10/2
; CURRENT APPLICATION NUMBER: US/11/264,558
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: US 10/312,184

; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/AU01/00729
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-264-558-38

Query Match 50.0%; Score 10; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 ACTTCTCAGA 20
||||| |||
Db 17 ACTTCTCAGA 8

RESULT 5
US-10-511-937-993
; Sequence 993, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 993
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-993

Query Match 49.0%; Score 9.8; DB 6; Length 20;
Best Local Similarity 84.6%; Pred. No. 6.2e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
||| ||| ||| ||| |||
Db 3 GCCCAGACTTCTC 15

RESULT 6
US-11-293-697-5435
; Sequence 5435, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28

; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5435
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-11-293-697-5435

Query Match 48.0%; Score 9.6; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CGCATAGACTTCTCA 18
| | | | | | | | | | | | | | | | | |
DB 1 CTGCTAGCCCTCTCA 16

RESULT 7
US-11-247-332-2
; Sequence 2, Application US/11247332
; Publication No. US20060094667A1
; GENERAL INFORMATION:
; APPLICANT: FUJIKURA, Hideki
; TITLE OF INVENTION: Glucopyranosyloxypyrazole Derivatives and Use Thereof in
; TITLE OF INVENTION: Medicines
; FILE REFERENCE: Q76132
; CURRENT APPLICATION NUMBER: US/11/247,332
; CURRENT FILING DATE: 2005-10-12
; PRIOR APPLICATION NUMBER: US/10/451,926
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: PCT/JP01/11348
; PRIOR FILING DATE: 2001-12-25
; PRIOR APPLICATION NUMBER: JPA 403534/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA primer
US-11-247-332-2

Query Match 48.0%; Score 9.6; DB 7; Length 20;
Best Local Similarity 75.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GCATAGACTTCTCAGA 20
| | | | | | | | | | | | | | | | | |
DB 2 GCATAGAGCCCCAGA 17

RESULT 8
US-11-251-465-371/c
; Sequence 371, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Bvgs, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 371
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-371

Query Match 46.0%; Score 9.2; DB 7; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCGCATAGACTT 14
| | | | | | | | | | | | | |
DB 15 GCCCGTGTAGACTT 2

RESULT 9
US-10-511-937-704
; Sequence 704, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 704
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-704

Query Match 46.0%; Score 9.2; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCGCATAGACTTC 15
| | | | | | | | | | | | | |
DB 6 ACCCGGAGACTTC 19

RESULT 10
US-10-469-938A-158
; Sequence 158, Application US/10469938A
; Publication No. US20060105329A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: Gene Panel for Genes Involving Liver Regeneration
; FILE REFERENCE: B68AYOP1331
; CURRENT APPLICATION NUMBER: US/10/469,938A
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: JP 2001-070940
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-469-938A-158

Query Match          46.0%; Score 9.2; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  ACCGCATAGACTTC 15
    |||||
DB   6  ACAGCATGTACTTC 19

RESULT 11
US-10-469-938A-63
; Sequence 63, Application US/10469938A
; Publication No. US20060105329A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: Gene Panel for Genes Involving Liver Regeneration
; FILE REFERENCE: B668AYOP1331
; CURRENT APPLICATION NUMBER: US/10/469,938A
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: JP 2001-070940
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-469-938A-63

Query Match          45.0%; Score 9; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  CGCATAGAC 12
    |||||
DB   3  CGCATAGAC 11

RESULT 12
US-11-251-465-201/c
; Sequence 201, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeginhte, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 201
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
```

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US-11-251-465-201

Query Match          45.0%; Score 9; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10  GACTTCTCA 18
    |||||
DB   11  GACTTCTCA 3

RESULT 13
US-11-233-507-18
; Sequence 18, Application US/11233507
; Publication No. US20060099616A1
; GENERAL INFORMATION:
; APPLICANT: Ommen van, Garrit-Jan B.
; APPLICANT: Deutekom van, Judith C.T.
; APPLICANT: Dennen den, Johannes T.
; APPLICANT: Aartsma-Rus, Annemieke
; TITLE OF INVENTION: Modulation of exon recognition in pre-mRNA by
; TITLE OF INVENTION: interfering with the secondary RNA structure
; FILE REFERENCE: P63917US00
; CURRENT APPLICATION NUMBER: US/11/233,507
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: PCT/NL2004/00196
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT PCT/NL03/00214
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: h42AON2
US-11-233-507-18

Query Match          44.0%; Score 8.8; DB 7; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  6  CATAGACTTCTC 17
    |||||
DB   1  CAGAGACUCCUC 12

RESULT 14
US-10-521-008-6/c
; Sequence 6, Application US/10521008
; Publication No. US20060099175A1
; GENERAL INFORMATION:
; APPLICANT: Van Den Hazel, Bart
; APPLICANT: Jensen, Anne D.
; APPLICANT: Nygaard, Frank B.
; APPLICANT: Andersen, Kim V.
; TITLE OF INVENTION: Full-length Interferon Gamma Polypeptide Variants
; FILE REFERENCE: 16384US04
; CURRENT APPLICATION NUMBER: US/10/521,008
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/DK03/000426
; PRIOR FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sense upstream vector Primer
US-10-521-008-6
```

Query Match 44.0%; Score 8.8; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ATAGACTTCTCA 18
| | | | | | | | | |
Db 19 ATAGACTCTCCA 8

RESULT 15
US-10-524-399-14
; Sequence 14, Application US/10524399
; Publication No. US2006009591A1
; GENERAL INFORMATION:
; APPLICANT: KRAUSE, Andreas
; APPLICANT: NIESE, Detlef
; APPLICANT: RAULF, Friedrich
; APPLICANT: SCHERER, Andreas
; TITLE OF INVENTION: Diagnosis of chronic rejection
; FILE REFERENCE: 4-32608A
; CURRENT APPLICATION NUMBER: US/10/524,399
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/405,225
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer sequence
US-10-524-399-14

Query Match 44.0%; Score 8.8; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TAGACTTCTCAG 19
| | | | | | | | | |
Db 1 TGGCCTTCTCAG 12

Search completed: June 9, 2006, 02:12:47
Job time : 24 secs

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